The Paradigms They Are a-Changin':
Past, present and future of your favorite bacteria.

Damien P. Devos
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Sevilla, SP
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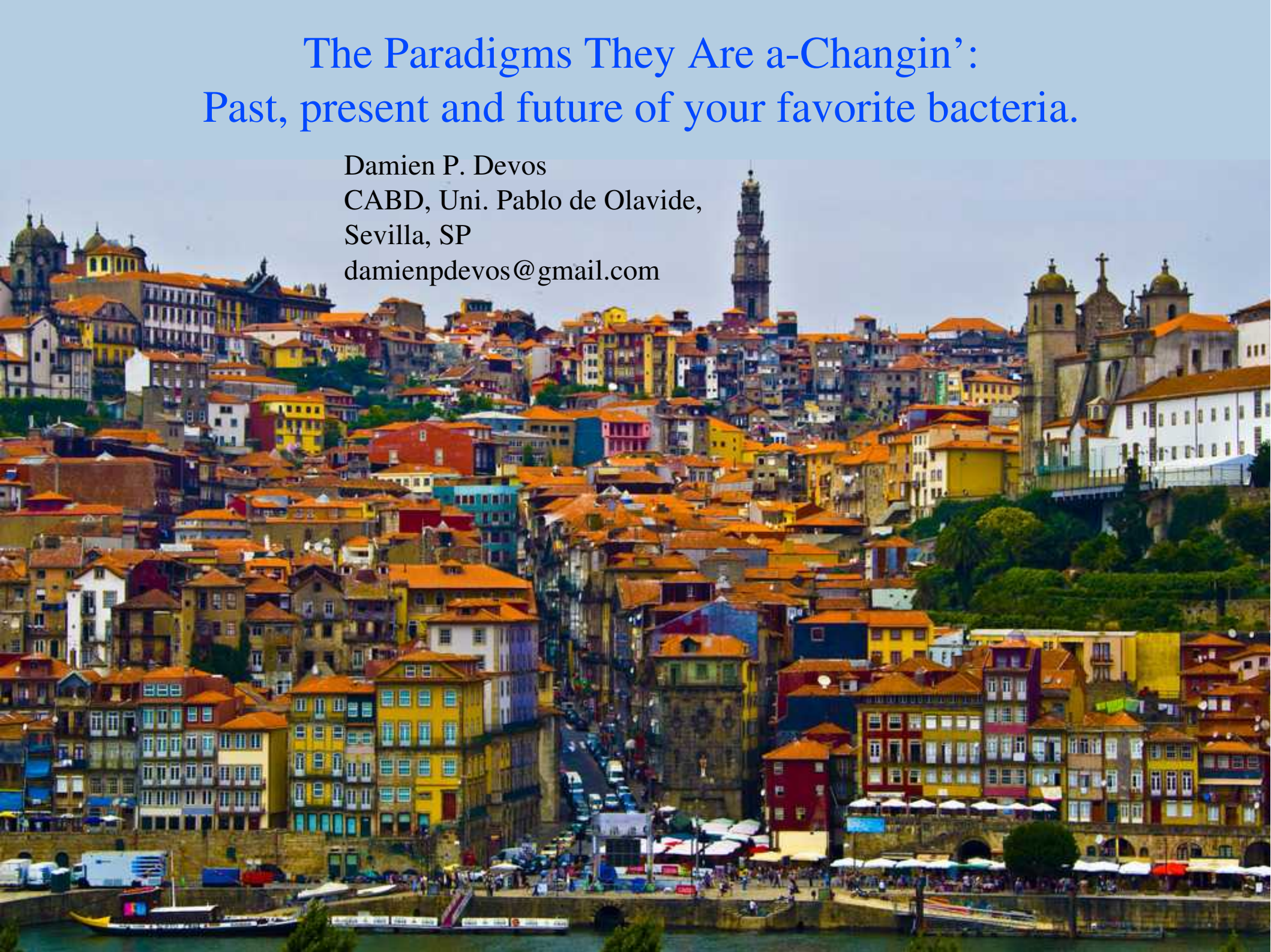

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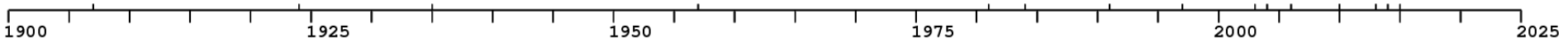
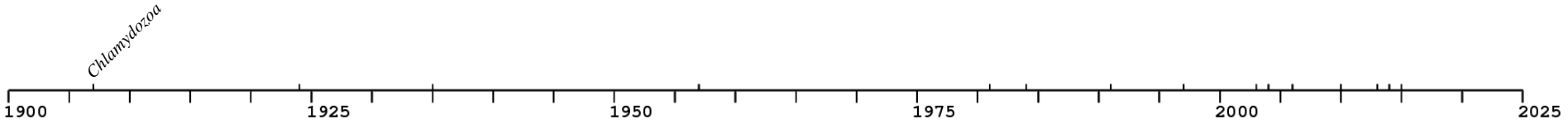
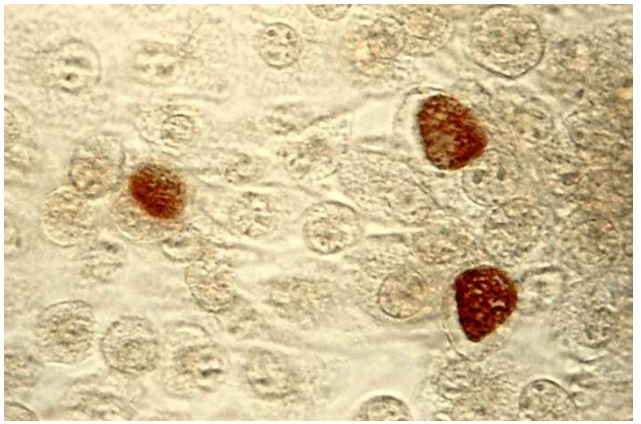


- My point of view and my own only!
- Totally biased

First, there was Chlamydia



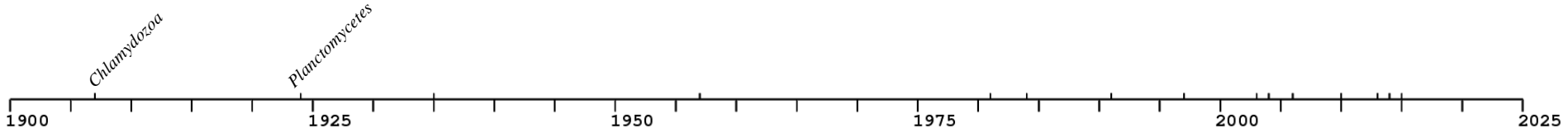


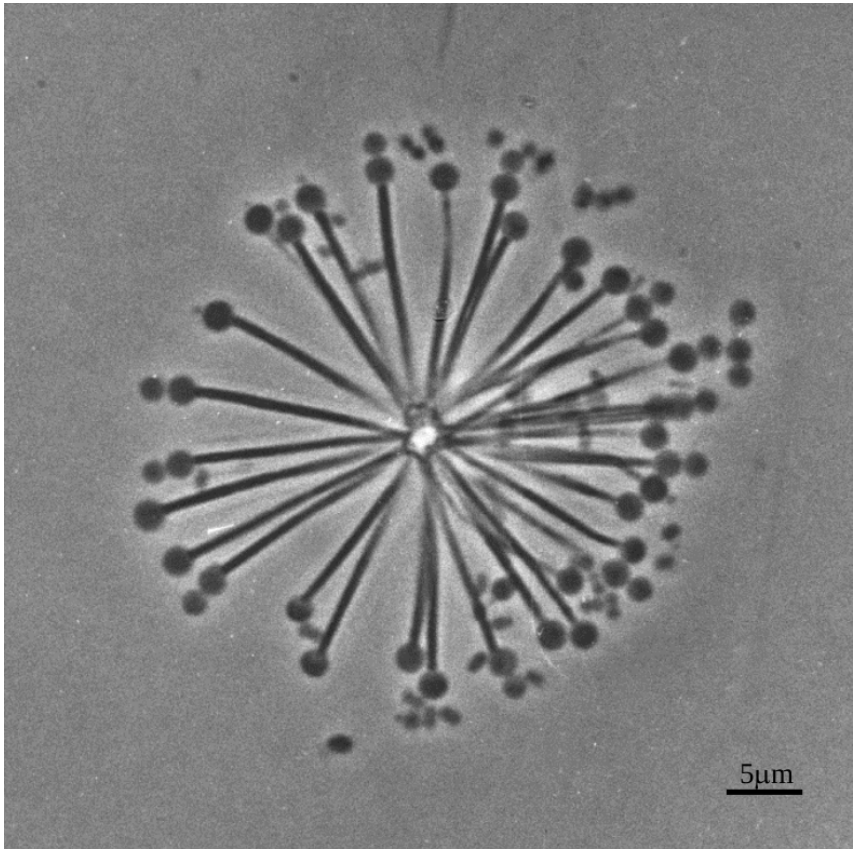
Halberstädter L, Prowazek SV. 1907. Über Zelleinschlüsse parasitärer Natur beim Trachom. Arbeiten aus dem Kaiserlichen Gesundheitsamte, Berlin 26:44–47.

"Chlamydozoa" (from the Greek word χλαμεσ, meaning mantle or cloak). **Originally considered neither protozoa nor bacteria and then regarded as viruses**, in the **1960s** they were recognized as bacteria. Later, these unique microorganisms were found to be among the most important bacterial pathogens of humankind. Halberstädter's and Prowazek's Chlamydozoa are now called *Chlamydia trachomatis*.

Horn, Ann Rev Micro 2008

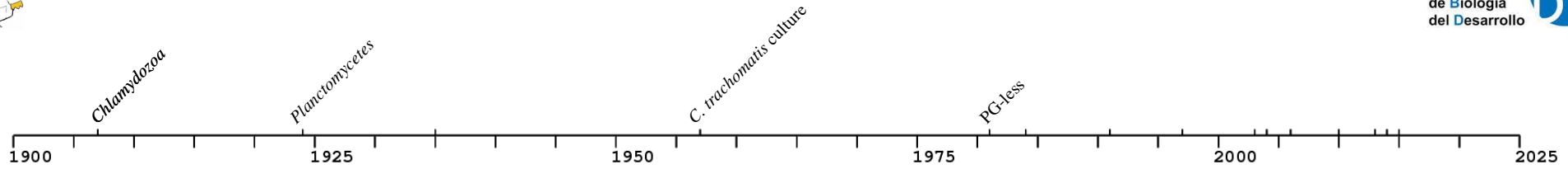
Then came *Planctomycetes*





Pl. Bekefii
Nandor Gimesi, 1924
Planctomycetes = floating fungi

PG-less bacteria



- No PG in Chlamydia (Caldwell *et al*., 81)
- No PG in Planctomyces, proteinaceus CW (Konig *et al*., 84)

Gemmata obscuriglobus

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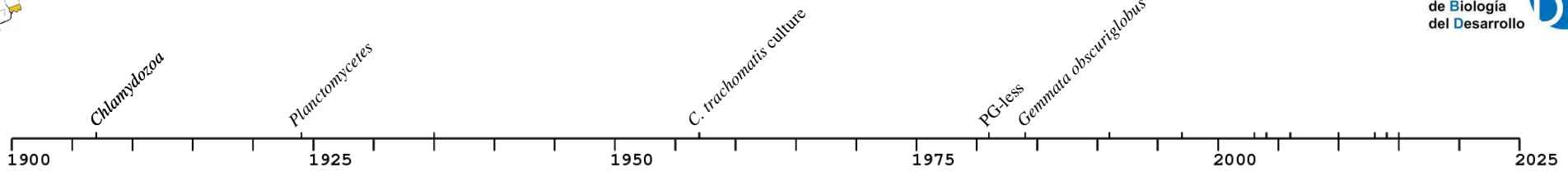
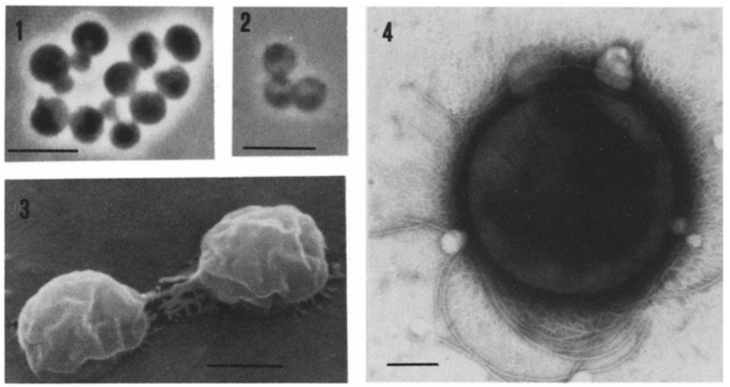




Antonie Van Leeuwenhoek. 1984;50(3):261-8.

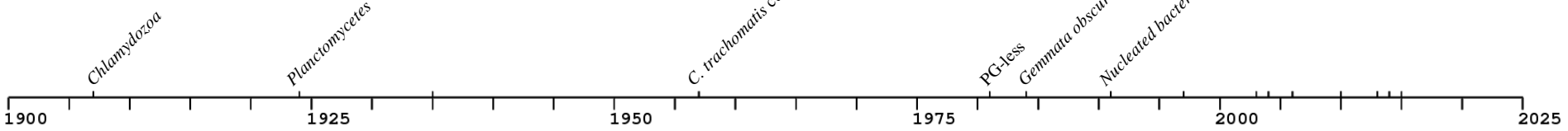
Gemmata obscuriglobus, a new genus and species of the budding bacteria.

Franzmann PD, Skerman VB.

Abstract

A single strain of a budding bacterium was isolated from freshwater. The strain had a life-cycle, with a multitrichous swarmer stage, and produced a phase-dark inclusion of packed ribosomes and nuclear material. The mol % G + C of the DNA was 64.4 +/- 1.0. A new genus, Gemmata with the type species Gemmata obscuriglobus is proposed. The type strain is UQM 2246.

The nucleated bacteria



Proc. Natl. Acad. Sci. USA
Vol. 88, pp. 8184–8188, September 1991
Cell Biology

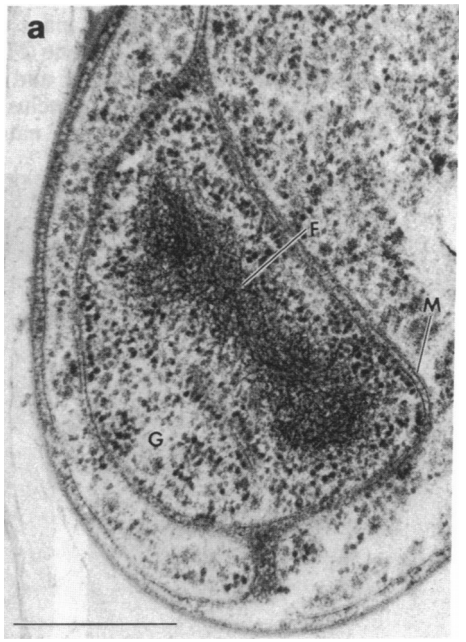
Membrane-bounded nucleoid in the eubacterium *Gemmata obscuriglobus*

(prokaryote/eukaryote distinction/electron microscopy)

JOHN A. FUERST* AND RICHARD I. WEBB

Department of Microbiology, University of Queensland, Brisbane, Queensland 4072, Australia

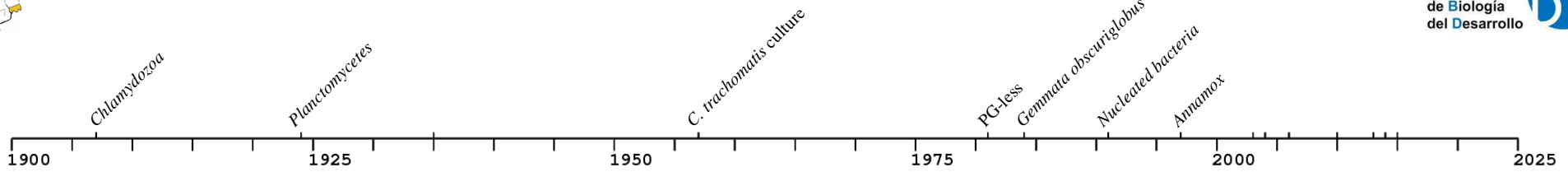
Communicated by Lynn Margulis, June 24, 1991



(Bar = 0.5 μm)

The occurrence of a membrane-bounded nucleoid in a eubacterial prokaryote is a significant exception to the evidence supporting the prokaryote/eukaryote dichotomous classification of cell structure.

Anammox discovery



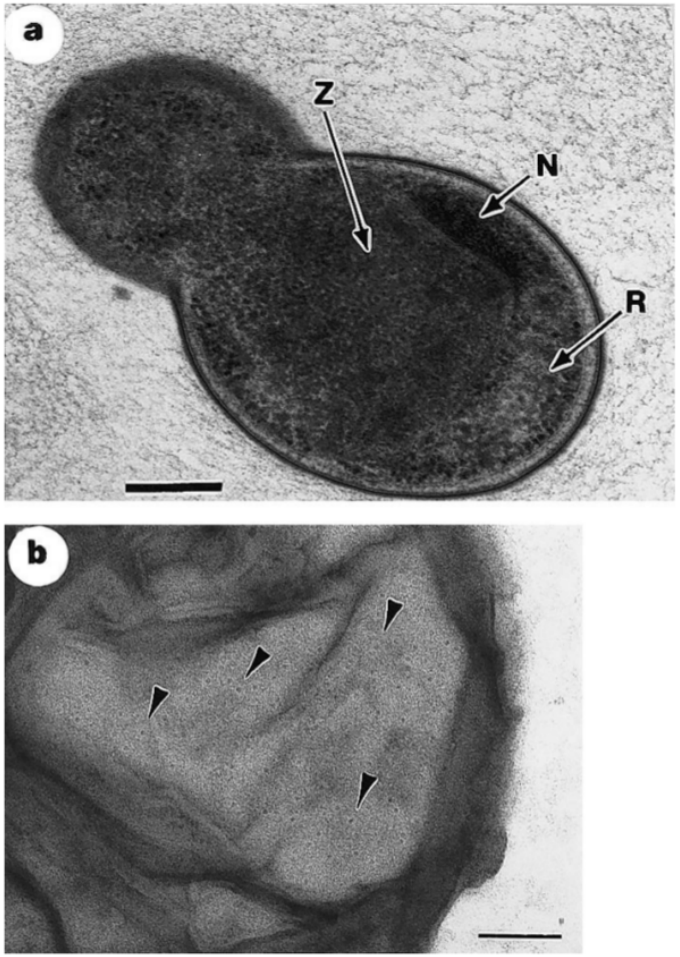
Missing lithotroph identified as new planctomycete

Marc Strous*, John A. Fuerst†, Evelien H. M. Kramer*, Susanne Logemann*, Gerard Muyzer‡, Katinka T. van de Pas-Schoonen*, Richard Webb†, J. Gijs Kuenen* & Mike S. M. Jetten*

** Department of Biotechnology, Delft University of Technology, Julianalaan 67, 2628 BC Delft, The Netherlands*
† Department of Microbiology & Parasitology and the Centre for Microscopy and Microanalysis, University of Queensland, Brisbane, Queensland 4072, Australia
‡ Netherlands Institute for Sea Research, 1790 AB Den Burg, The Netherlands

With the increased use of chemical fertilizers in agriculture, many densely populated countries face environmental problems associated with high ammonia emissions. The process of anaerobic ammonia oxidation ('anammox') is one of the most innovative technological advances in the removal of ammonia nitrogen from

NATURE | VOL 400 | 29 JULY 1999 | www.nature.com



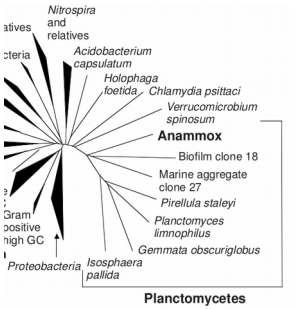


Figure 3 Phylogenetic position of the lithotroph responsible for anaerobic ammonium oxidation within the domain Bacteria, based on 16S rRNA phylogeny. The anammox bacterium represents a new, deep branch inside the order *Planctomycetales*.

Verrucomicrobia & Lentisphaerae

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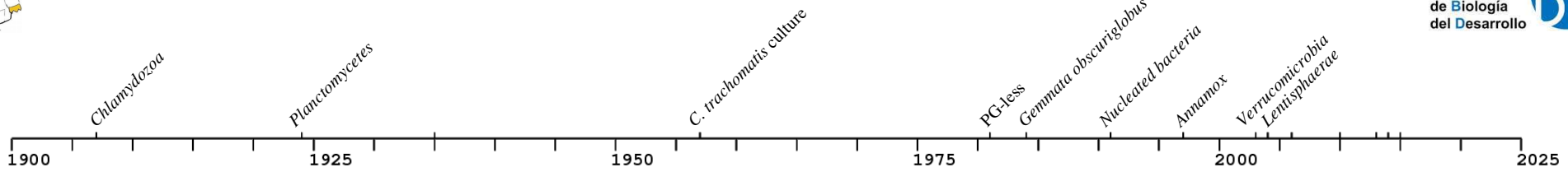


Int J Syst Evol Microbiol. 2003 Jan;53(Pt 1):211-5.

Victivallis vadensis gen. nov., sp. nov., a sugar-fermenting anaerobe from human faeces.

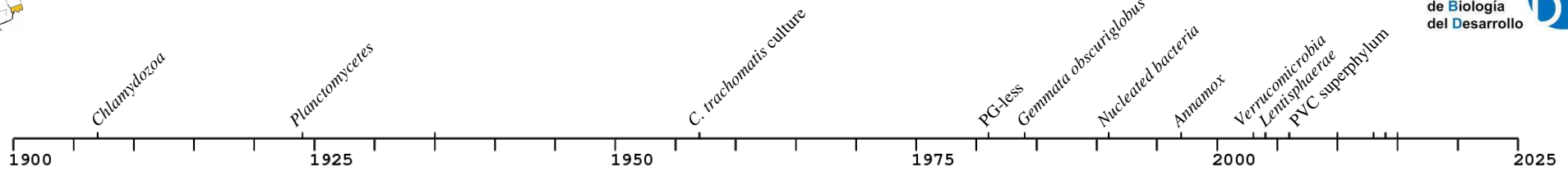
Zoetendal EG[1], Plugge CM, Akkermans AD, de Vos WM.

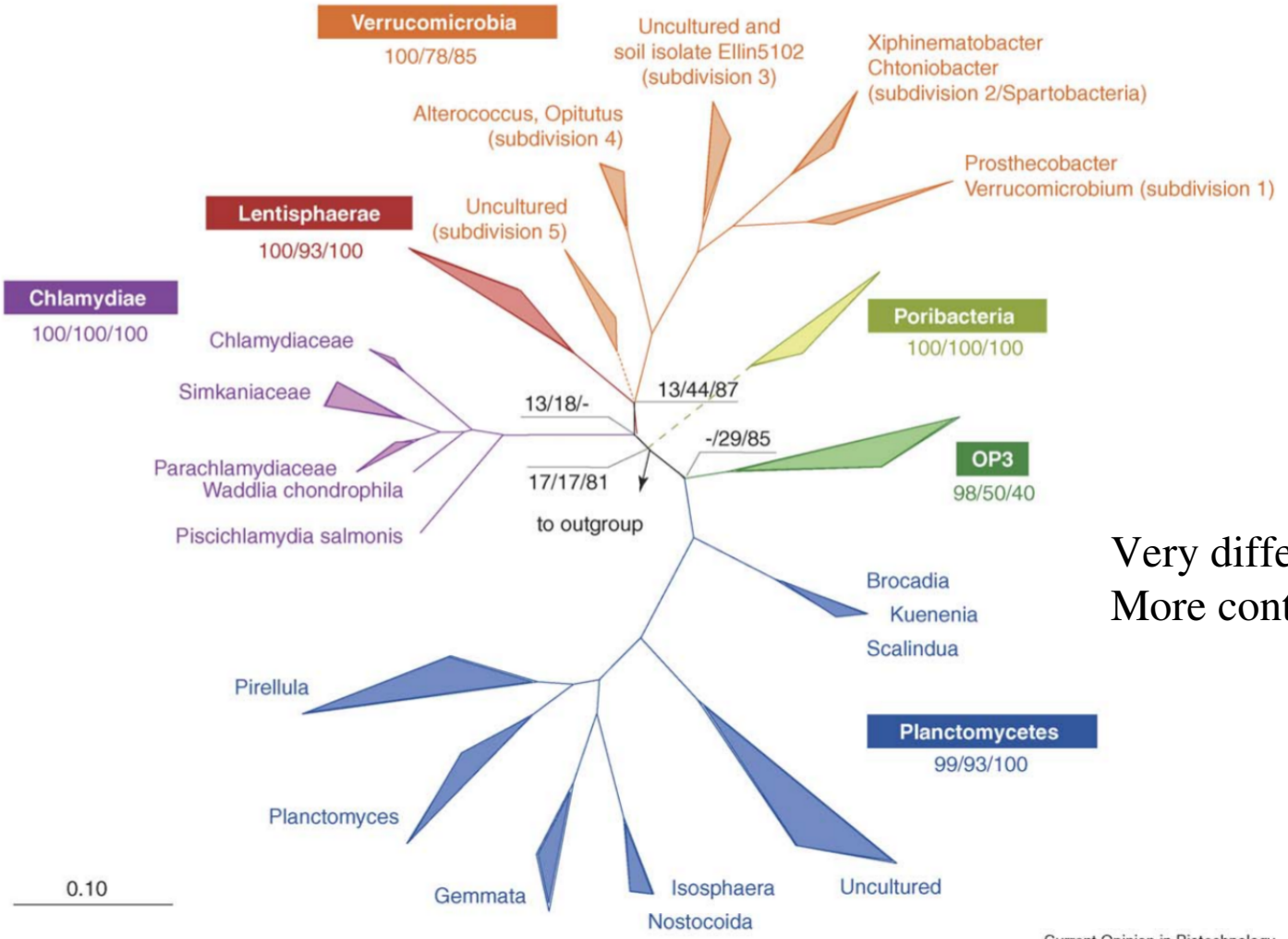
Environ Microbiol. 2004 Jun;6(6):611-21.

Lentisphaera araneosa gen. nov., sp. nov, a transparent exopolymer producing marine bacterium, and the description of a novel bacterial phylum, Lentisphaerae.

Cho JC[1], Vergin KL, Morris RM, Giovannoni SJ.

The PVC superphylum



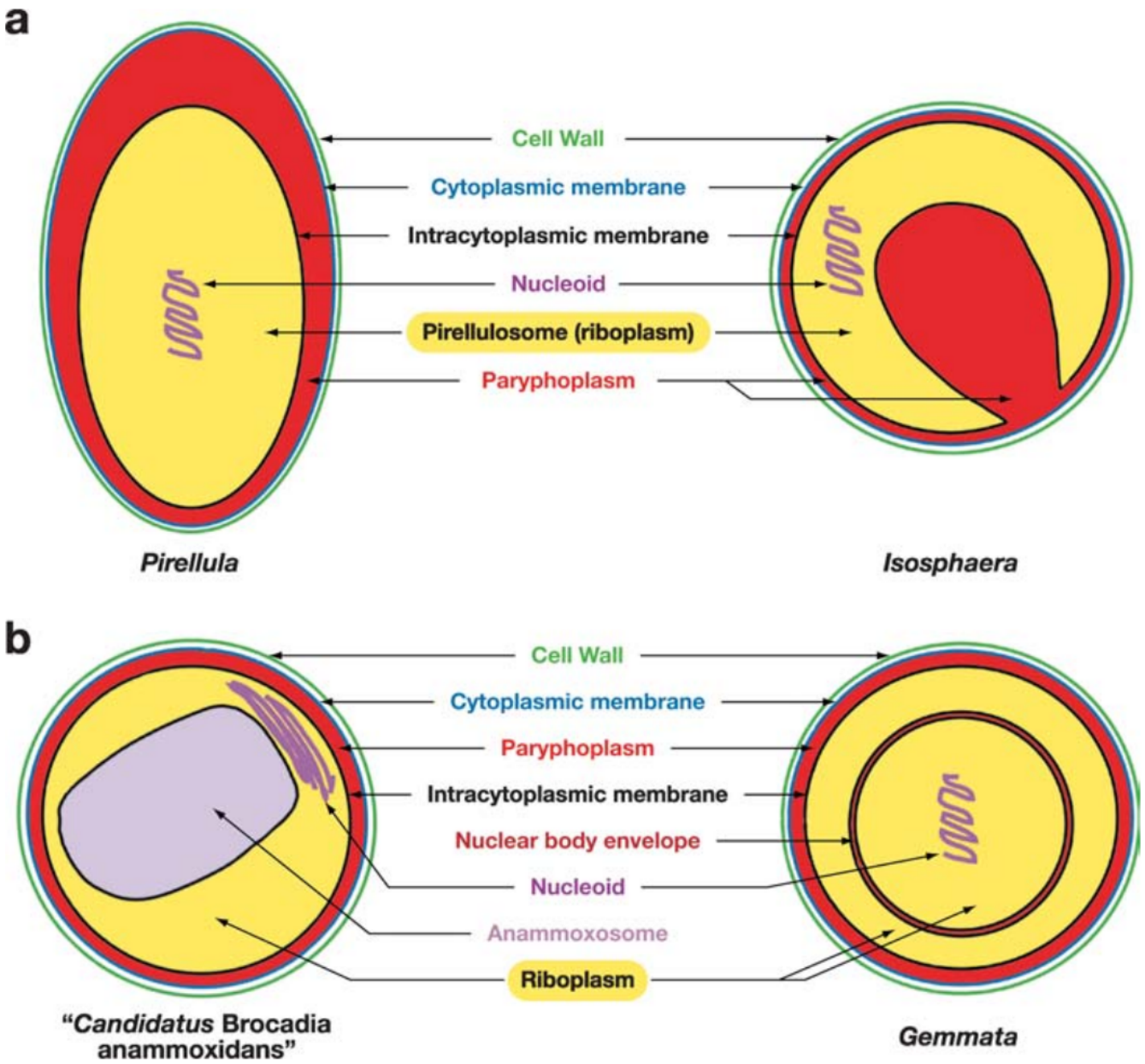


Very different organism
More controversy!

Current Opinion in Biotechnology

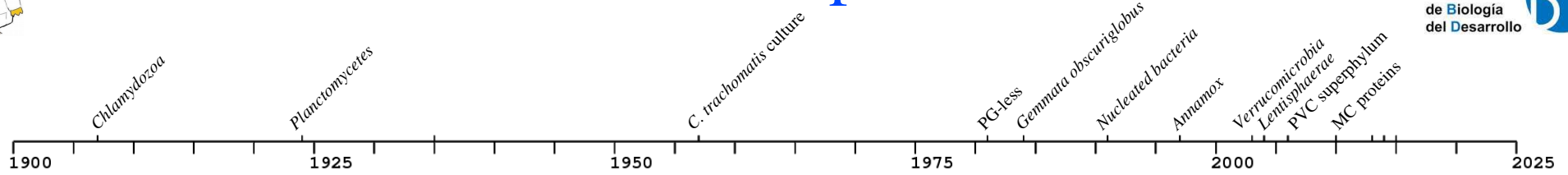
Wagner and Horn (2006)

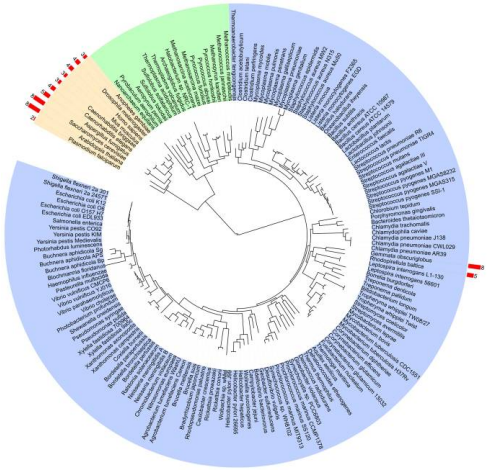
3rd cell plan

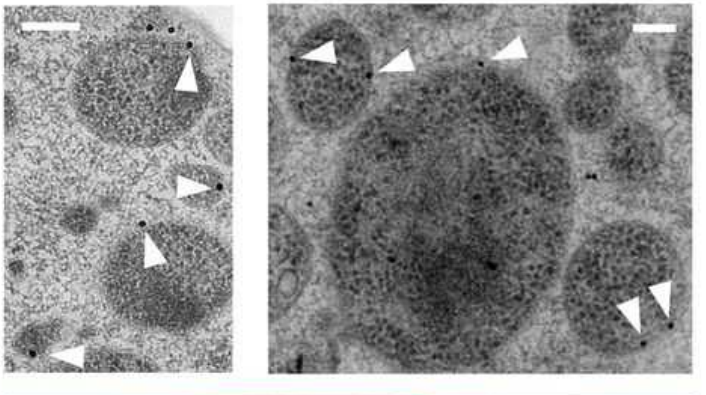


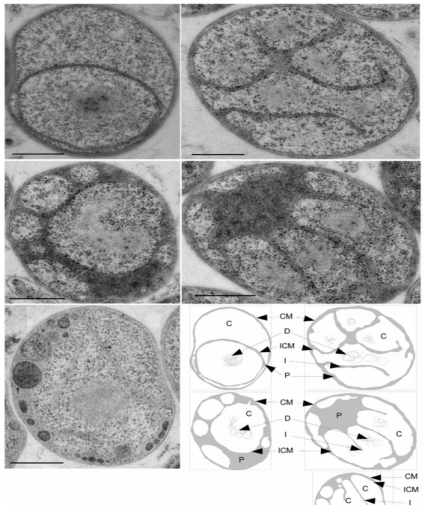
Fuerst, Ann Rev Micro 2005

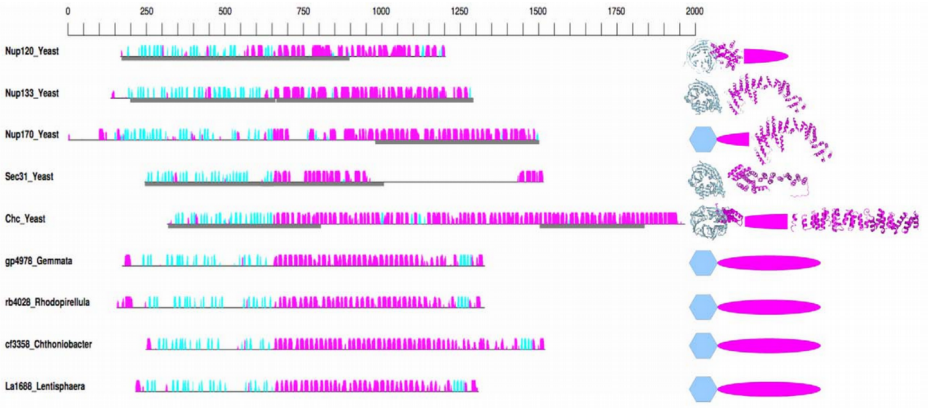
Membrane coat like proteins in PVCs





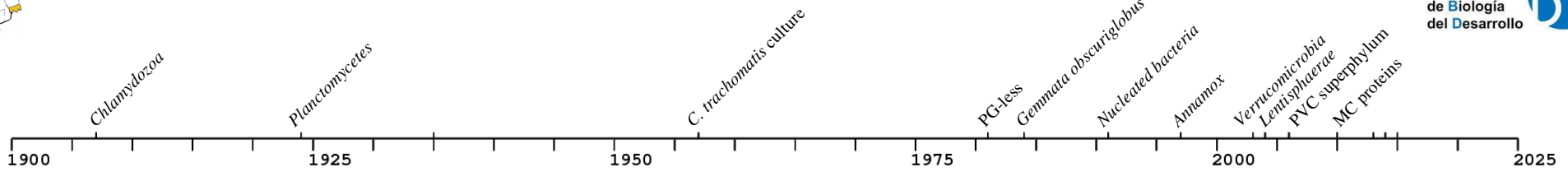


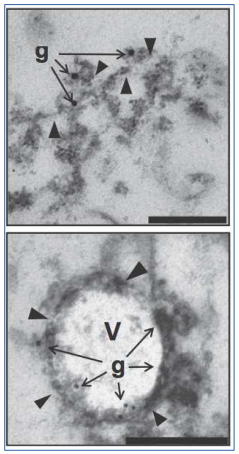


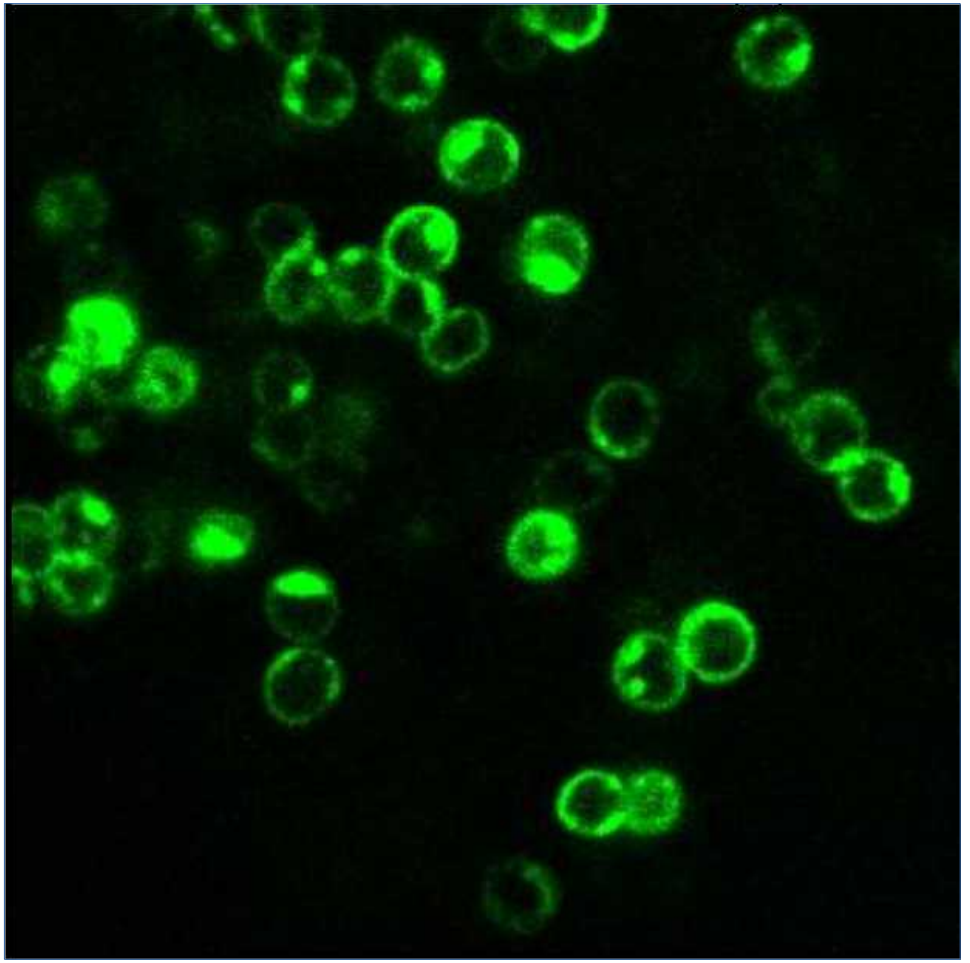


Santarella *et* al., PLoS B 2010

Prokaryotic endocytosis?

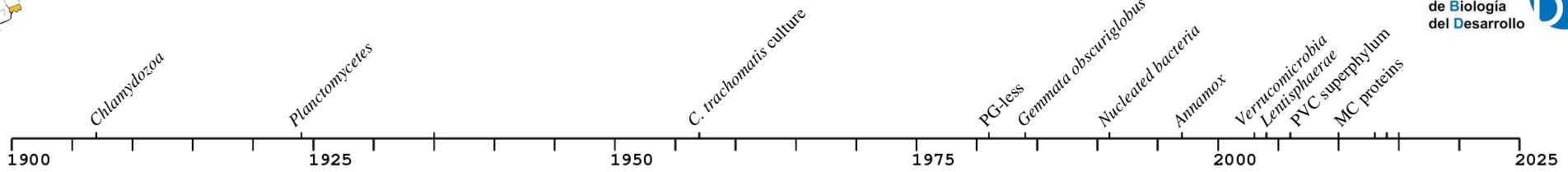






Lonhienne *et* al., PNAS 2010

Controversy up to ~2013



- PG-less
- FtsZ-less
- Nucleated bacteria
- Membrane system, Membrane coat proteins, Endocytosis
- Melting pot of very different bacteria
- 3rd cell plan, not G-, not G+

Frontiers SI 2012-13

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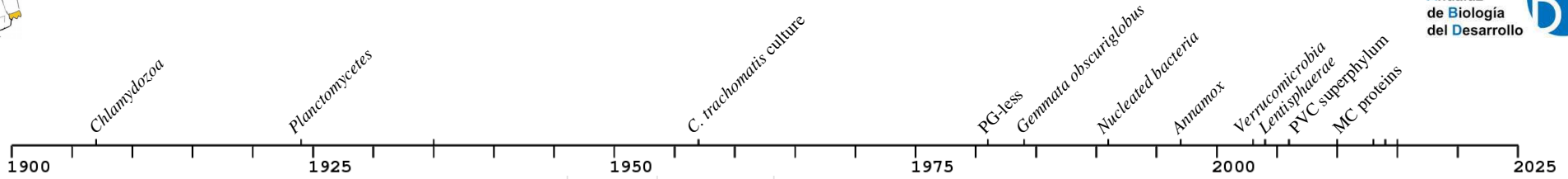
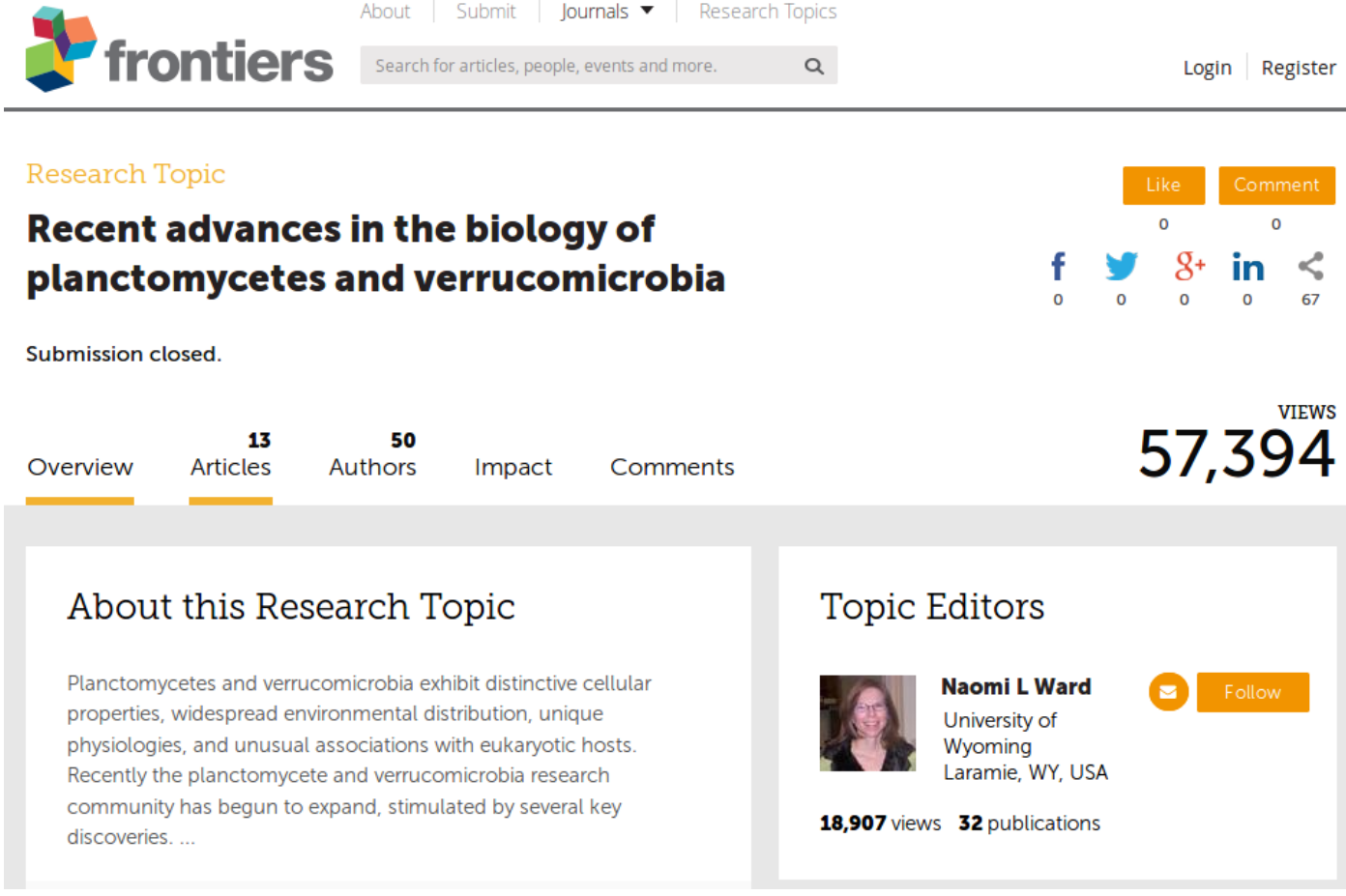
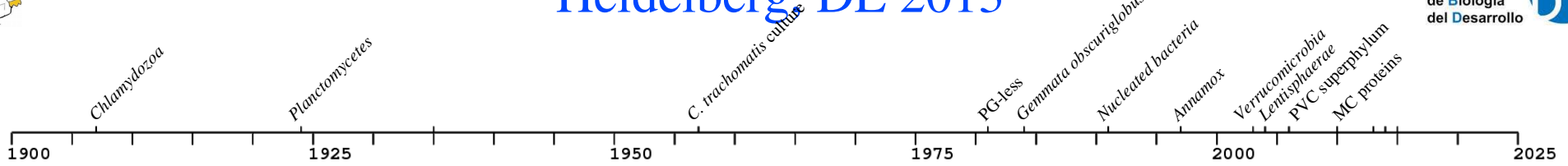




13 articles, 50 authors

1st PVC meeting
Heidelberg, DE 2013



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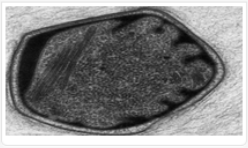
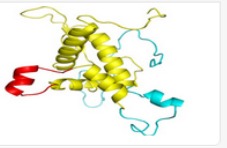
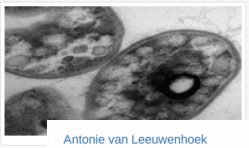
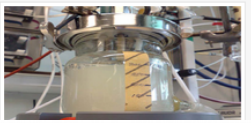
EMBO Workshop

Planctomycetes-Verrucomicrobia-Chlamydiae Superphylum: Exceptions to the bacterial definition?

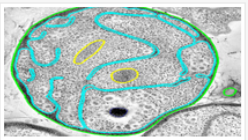
28 February - 2 March, 2013 | Heidelberg, Germany

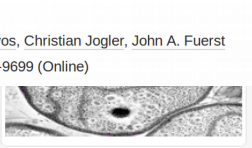
HOME ORGANISERS SPEAKERS PROGRAMME VENUE TRANSPORT REGISTRATION

ABOUT THE WORKSHOP

The *Planctomycetes-Verrucomicrobia-Chlamydiae* (PVC) superphylum is an assemblage
with different data and phylogeny estimation methods. This EMBO workshop will be the fi
the PVC members. The Workshop will bring together researchers working on such bacteri
and evolutionary scenarios. *(read more...)*



Antonie van Leeuwenhoek
All Volumes & Issues

Volume 104, Issue 4, October 2013

Special Issue on Papers from the 1st EMBO workshop on the Planctomycetes-Verrucomicrobia-Chlamydiae superphylum: Exceptions to the bacterial definition?

Issue Editors: Damien P Devos, Christian Jogler, John A. Fuerst
ISSN: 0003-6072 (Print) 1572-9699 (Online)

14 articles, ~30 authors

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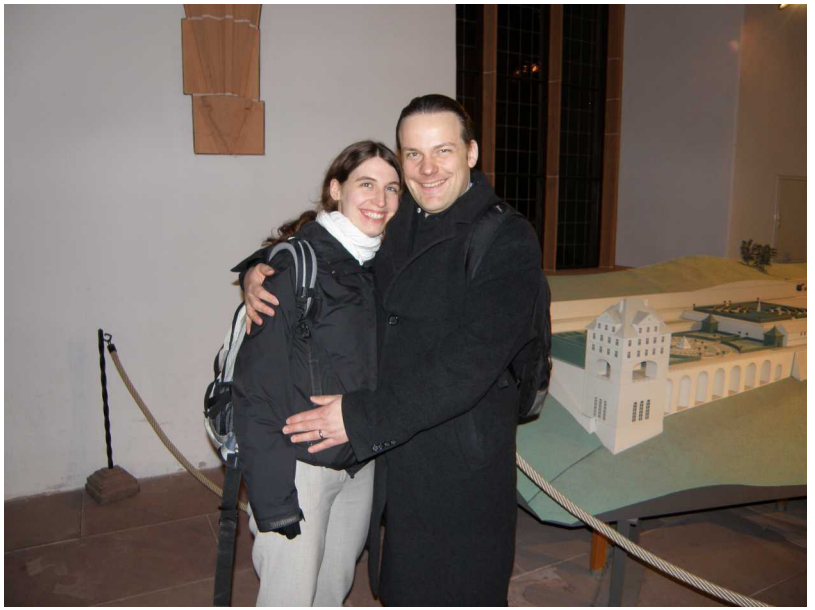
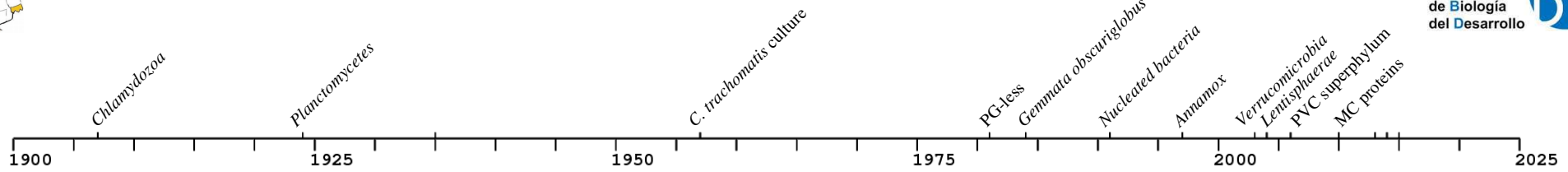
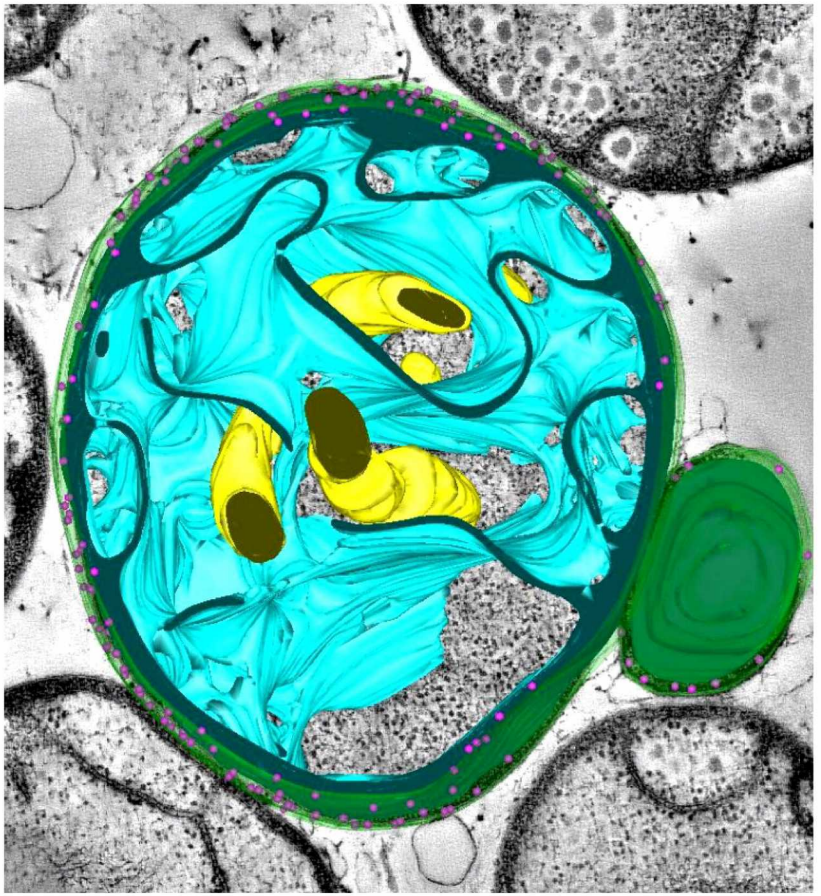
PVC



Gemmata 3D reconstruction

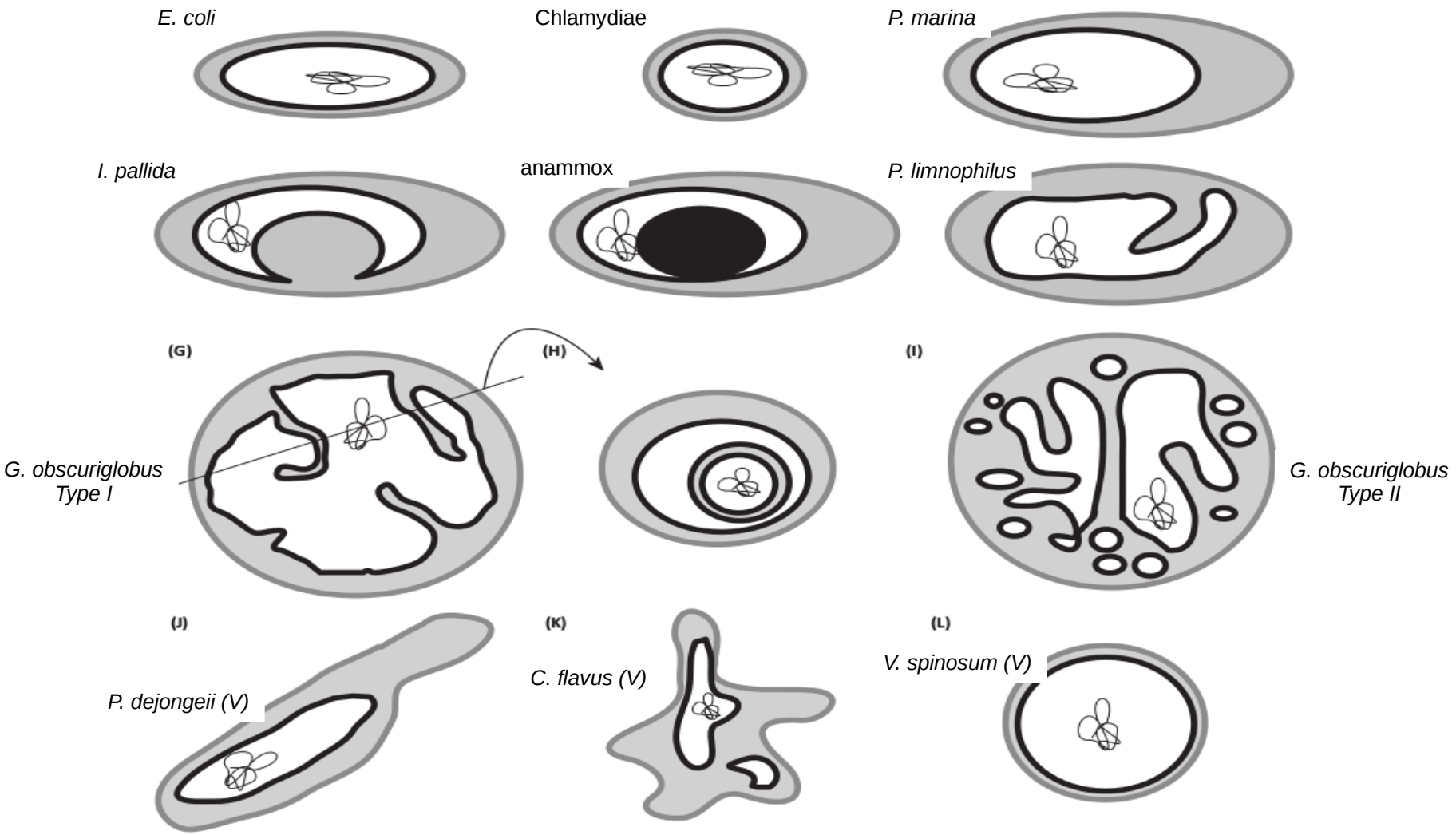


Sections 250nm
Technai F30 300kv (FEI)
Dual axis tilt series
IMOD
1130 slices/5



Santarella *et al.*, PLoS B 2010

Variation of, but no exception to, Gram(-) cell plan



PG in PVC

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Nat Commun. 2015 May 12;6:7116. doi: 10.1038/ncomms8116.

Planctomycetes do possess a peptidoglycan cell wall.

Jeske O[1], Schüler M[2], Schumann P[3], Schneider A[4], Boedeker C[1], Jogler M[1], Bollschweiler D[2], Rohde M[5], Mayer C[4], Engelhardt H[2], Spring S[3], Jogler C[1].

Nat Commun. 2015 May 12;6:6878. doi: 10.1038/ncomms7878.

Anammox Planctomycetes have a peptidoglycan cell wall.

van Teeseling MC[1], Mesman RJ[1], Kuru E[2], Espaillat A[3], Cava F[3], Brun YV[4], VanNieuwenhze MS[5], Kartal B[6], van Niftrik L[1].

Front Microbiol. 2017 Feb 13;8:202. doi: 10.3389/fmicb.2017.00202. eCollection 2017.

Three Novel Species with Peptidoglycan Cell Walls form the New Genus Lacunisphaera gen. nov. in the Family Opitutaceae of the Verrucomicrobial Subdivision 4.

Rast P[1], Glöckner I[2], Boedeker C[1], Jeske O[1], Wiegand S[1], Reinhardt R[3], Schumann P[4], Rohde M[5], Spring S[6], Glöckner FO[7], Jogler C[8], Jogler M[1].

2nd PVC meeting
Sevilla, SP 2015

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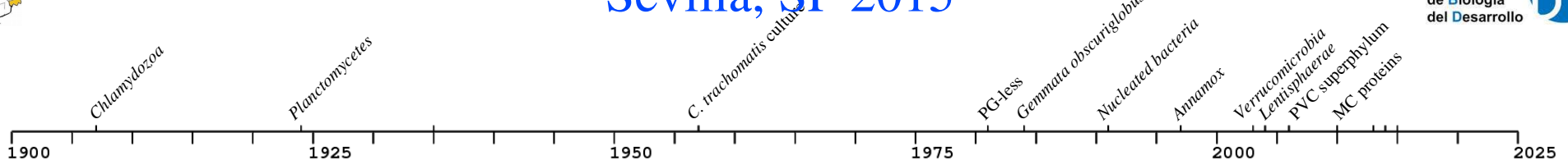
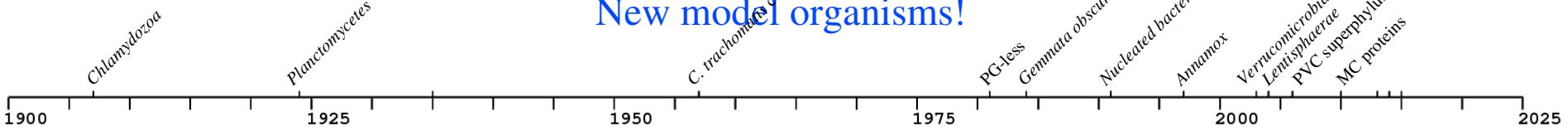


Special Issue
Frontiers

Frontiers SI

Planctomycetes-Verrucomicrobia-Chlamydiae bacterial superphylum: New model organisms!



- 12 articles
- 86 authors
- 13 countries
  - Netherlands, Portugal, USA, Malaysia, UK, Germany, Switzerland, Austria, Spain, France, Finland, Greece, New Zealand

Frontiers SI

Planctomycetes-Verrucomicrobia-Chlamydiae bacterial superphylum: New model organisms!

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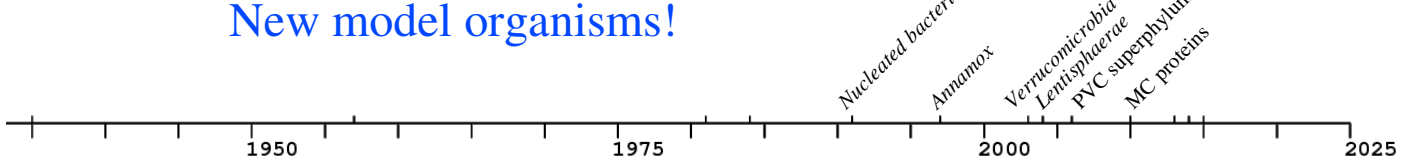
Ca. Similichlamydia in Epitheliocystis Co-infection of Gilthead Seabream Gills: Unique Morphological Features of a Deep Branching Chlamydial Family

Helena M. B. Seth-Smith, Pantelis Katharios, Nancy Dourala, José M. Mateos, Alexander G. J. Fehr, Lisbeth Nufer, Maja Ruetten, Maricruz Guevara Soto and Lloyd Vaughan

316 total views



Planctomycetes as Novel Source of Bioactive Molecules

Ana P. Graça, Rita Calisto and Olga M. Lage

Developing Techniques for the Utilization of Planctomycetes As Producers of Bioactive Molecules

Olga Jeske, Frank Surup, Marcel Kettenis, Patrick Rast, Birthe Förster, Mareike Jogler, Joachim Wink and Christian Jogler

Untangling Genomes of Novel Planctomycetal and Verrucomicrobial Species from Monterey Bay Kelp Forest Metagenomes by Refined Binning

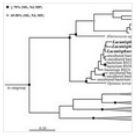
John Vollmers, Martinique Frentrup, Patrick Rast, Christian Jogler and Anne-Kristin Kaster

Development of Genetic Tools for the Manipulation of the Planctomycetes

Elena Rivas-Marín, Inés Canosa, Eduardo Santero and Damien P. Devos

Fuerstia marisgermanicae gen. nov., sp. nov., an Unusual Member of the Phylum Planctomycetes from the German Wadden Sea

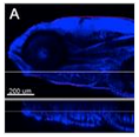
Timo Kohn, Anja Heuer, Mareike Jogler, John Vollmers, Christian Boedeker, Boyke Bunk, Patrick Rast, Daniela Borchert, Ines Glöckner, Heike M. Freese, Hans-Peter Klenk, Jörg Overmann, Anne-Kristin Kaster, Manfred Rohde, Sandra Wiegand and Christian Jogler



Three Novel Species with Peptidoglycan Cell Walls form the New Genus Lacunisphaera gen. nov. in the Family Opitutaceae of the Verrucomicrobial Subdivision

4

Patrick Rast, Ines Glöckner, Christian Boedeker, Olga Jeske, Sandra Wiegand, Richard Reinhardt, Peter Schumann, Manfred Rohde, Stefan Spring, Frank O. Glöckner, Christian Jogler and Mareike Jogler

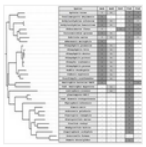


A Zebrafish Model for Chlamydia Infection with the Obligate Intracellular Pathogen Waddlia chondrophila

Alexander G. J. Fehr, Maja Ruetten, Helena M. B. Seth-Smith, Lisbeth Nufer, Andrea Voegtlin, Angelika Lehner, Gilbert Greub, Philip S. Crosier, Stephan C. F. Neuhauss and Lloyd Vaughan

Characterization of Outer Membrane Proteome of Akkermansia muciniphila Reveals Sets of Novel Proteins Exposed to the Human Intestine

Noora Ottman, Laura Huuskonen, Justus Reunanen, Sjef Boeren, Judith Klievink, Hauke Smidt, Clara Belzer and Willem M. de Vos



Evolutionary Cell Biology of Division Mode in the Bacterial Planctomycetes-Verrucomicrobia- Chlamydiae Superphylum

Elena Rivas-Marín, Inés Canosa and Damien P. Devos

The S-Layer Protein of the Anammox Bacteriu Kuenenia stuttgartiensis Is Heavily O-Glycosylated

Muriel C. F. van Teeseling, Daniel Maresch, Cornelia B. Rat Rudolf Figl, Friedrich Altmann, Mike S. M. Jetten, Paul Messner, Christina Schäffer and Laura van Niftrik

Identification and Partial Characterization of a Novel UDP-N-Acetylenolpyruvoylglucosamine Reductase/UDP-N-Acetylmuramate:l-Alanine Ligase Fusion Enzyme from Verrucomicrobium spinosum DSM 4136T

Kubra F. Naqvi, Delphine Patin, Matthew S. Wheatley, Michael A. Savka, Renwick C. J. Dobson, Han Ming Gan, Hélène Barreteau, Didier Blanot, Dominique Mengin-Lecreulx and André O. Hudson

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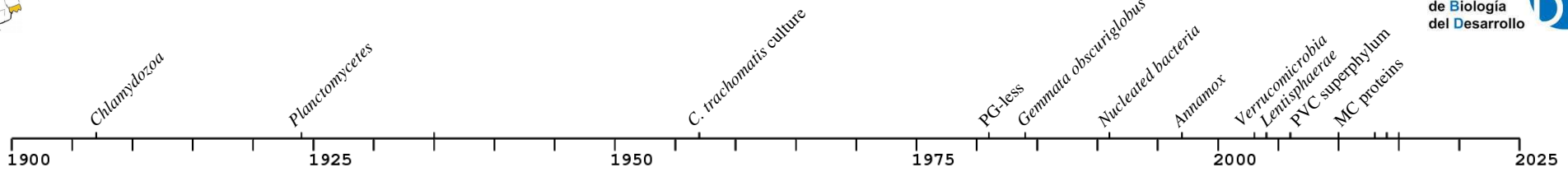
frontiers
Research Topics

Damien Paul Devos,
The Research Topic you recently contributed to is attracting interest from the community, below you can see its current impact numbers.

Planctomycetes-Verrucomicrobia-Chlamydiae bacterial superphylum: New model organisms!

	12	ARTICLES
	16,090	TOTAL VIEWS
	1,875	DOWNLOADS
	45	SHARES

Resolving the controversies



Superphylum status now amply accepted
Variation of Gram – cell plan
PG present

Pubmed & genomes trends

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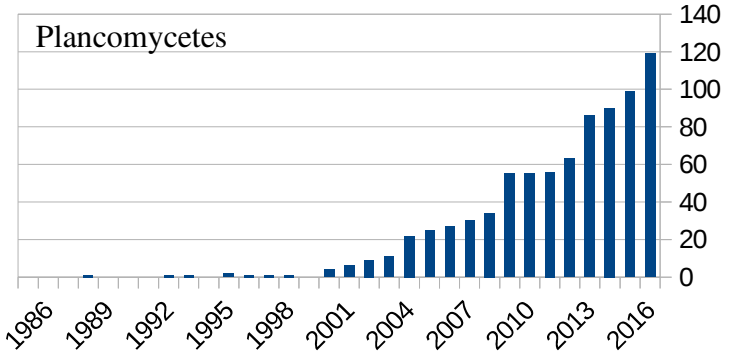

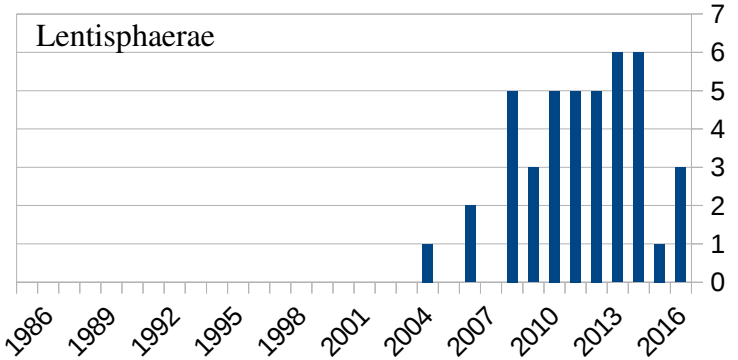

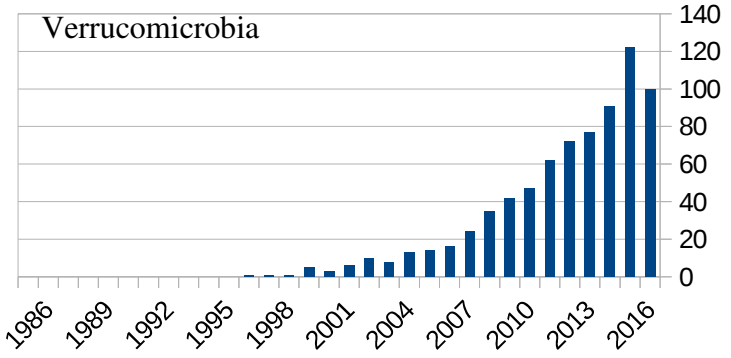

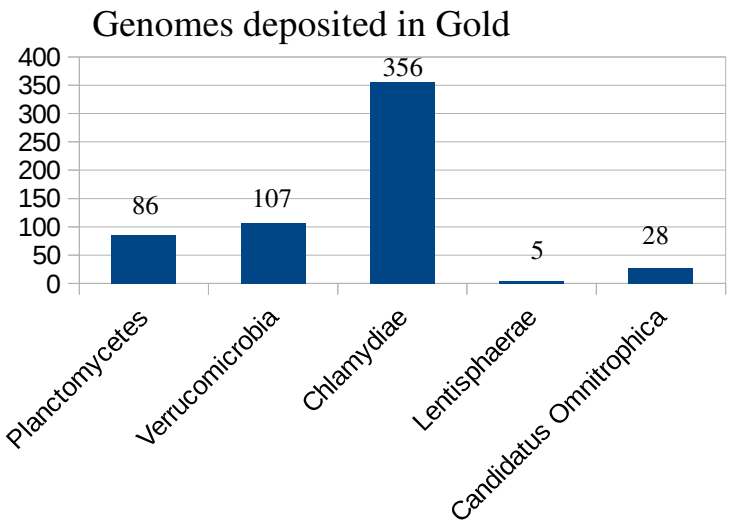

Alexandru Dan Corlan. Medline trend: automated yearly statistics of PubMed results for any query, 2004. Web resource at URL:http://dan.corlan.net/medline-trend.html.

PVC bacteria: New model organisms!

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Ecology and biotechnology:

- Carbon and nitrogen cycle on earth
- Methane oxidation (anammox)
- Biomolecules
- Antibiotics

Human health:

- Chlamydiae
- Verrucomicrobia
  - gastrointestinal homeostasis
  - Immune system
  - Cell development
  - Obesity
- Planctomycetes

Mind the PVCs.

Devos DP, Ward NL.

Environ Microbiol. 2014 May;16(5):1217-21. doi: 10.1111/1462-2920.12349.

PMID: 24750535 [PubMed - indexed for MEDLINE]

Evolutionary cell biology:

- Deviate from 'classical' bacteria characters and definition
- Origin of those characters

PVC genetic tools

Centro Andaluz de Biología del Desarrollo

Characterization of Planctomyces limnophilus and development of genetic tools for its manipulation establish it as a model species for the phylum Planctomycetes.

Jogler C, Glöckner FO, Kolter R.

Appl Environ Microbiol. 2011 Aug 15;77(16):5826-9. doi: 10.1128/AEM.05132-11.

Random transposon mutagenesis of Verrucomicrobium spinosum DSM 4136(T).

Domman DB, Steven BT, **Ward NL**.

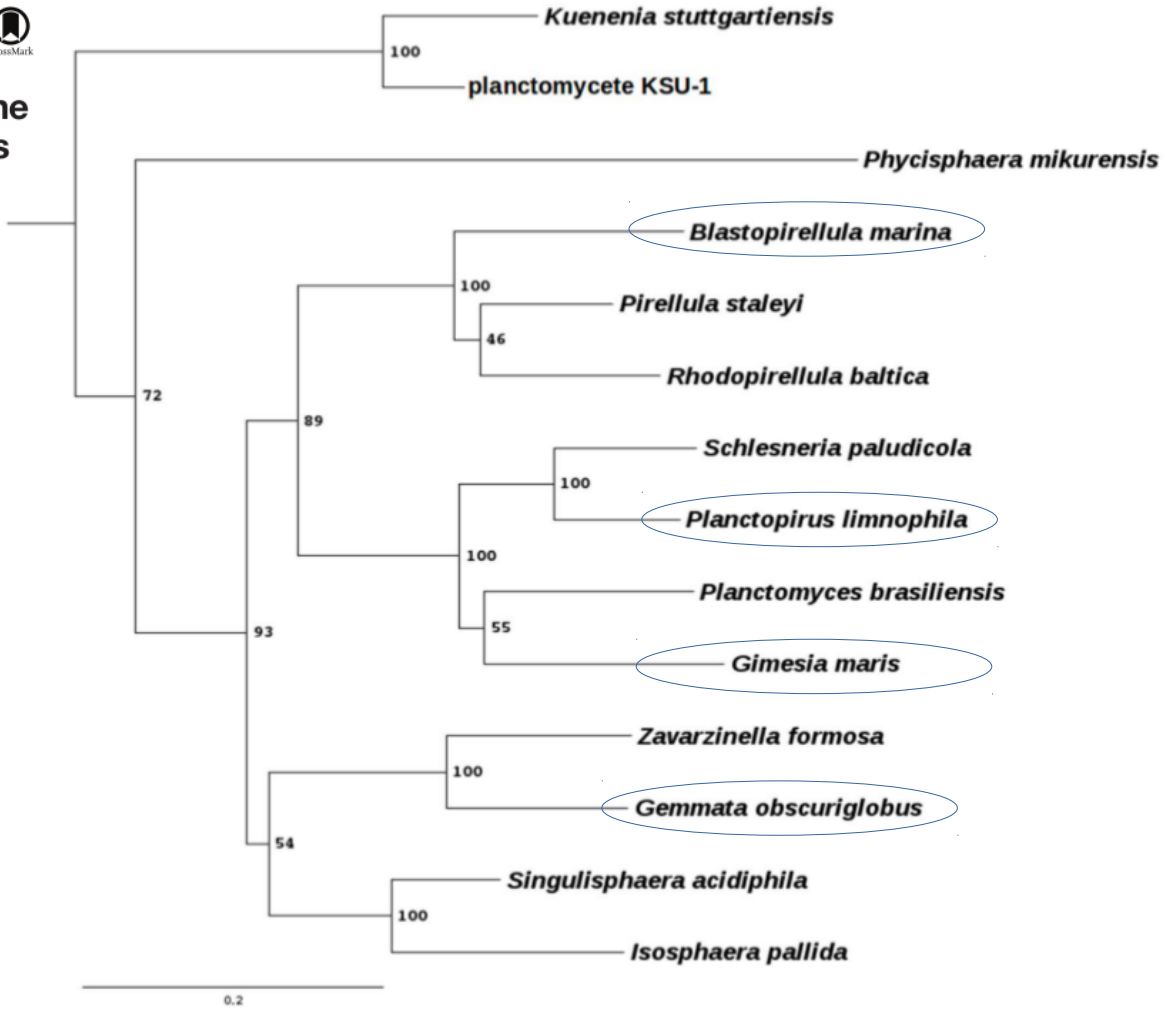
Arch Microbiol. 2011 Apr;193(4):307-12. doi: 10.1007/s00203-010-0666-5.

frontiers in Microbiology

ORIGINAL RESEARCH
published: 16 June 2016
doi: 10.3389/fmicb.2016.00914

Development of Genetic Tools for the Manipulation of the Planctomycetes

*Elena Rivas-Marín[1], Inés Canosa[2], Eduardo Santero[2] and Damien P. Devos[1]**



Characterization of a planctomycetal organelle: a novel bacterial microcompartment for the aerobic degradation of plant saccharides.

Erbilgin O, McDonald KL, Kerfeld CA.

Appl Environ Microbiol. 2014 Apr;80(7):2193-205. doi: 10.1128/AEM.03887-13.

Transposon mutagenesis of Planctomyces limnophilus and analysis of a pckA mutant.

Schreier HJ, Dejtisakdi W, Escalante JO, Brailo M.

Appl Environ Microbiol. 2012 Oct;78(19):7120-3. doi: 10.1128/AEM.01794-12.

Happening right now!

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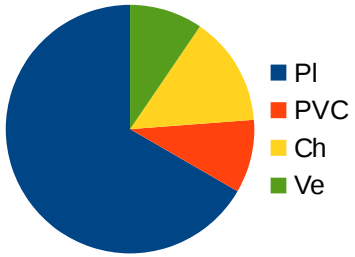
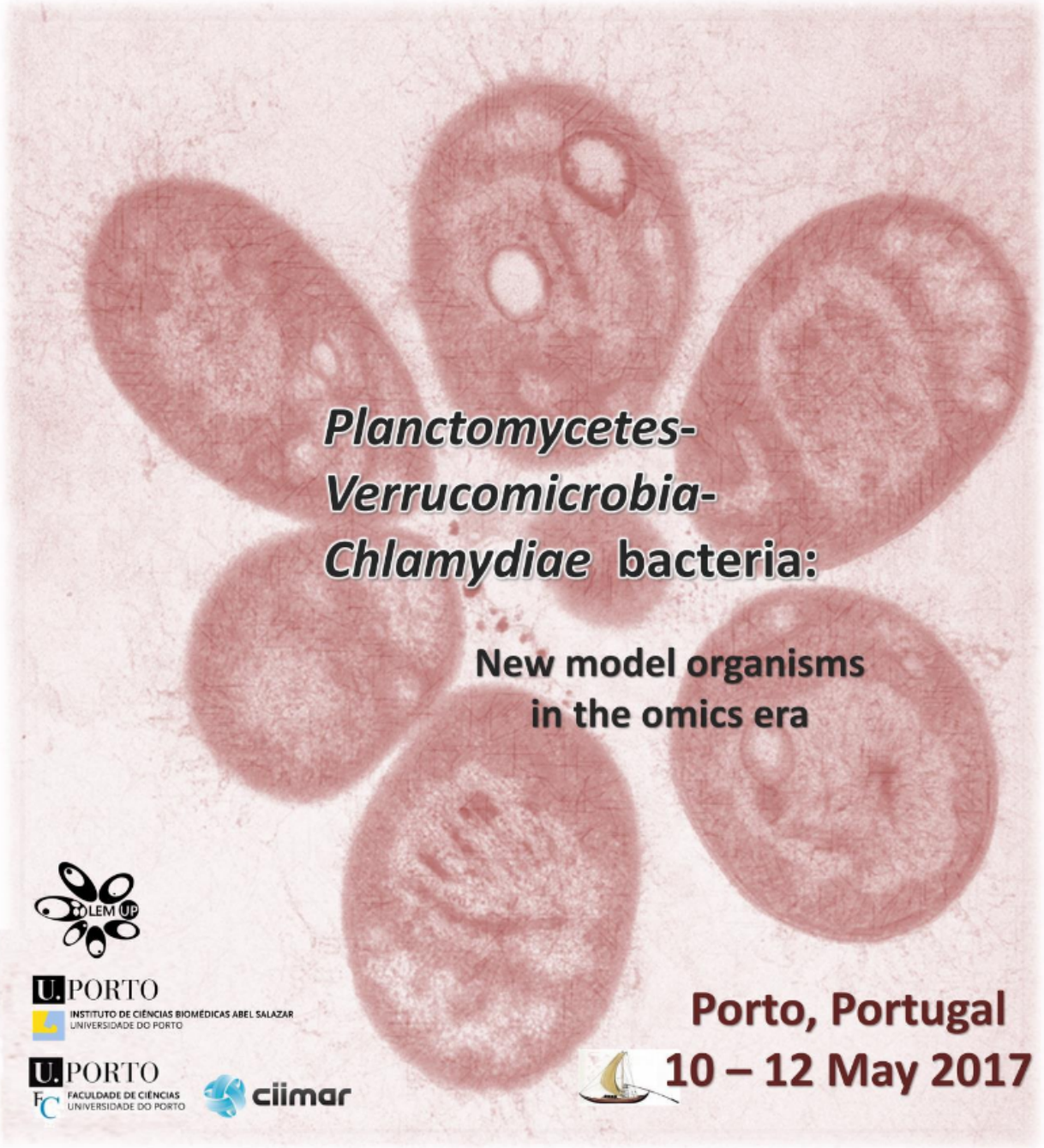
3x researchers
10 countries
21 talks





The future is bright!

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Let’s ask for money!

Open Questions & Future Research

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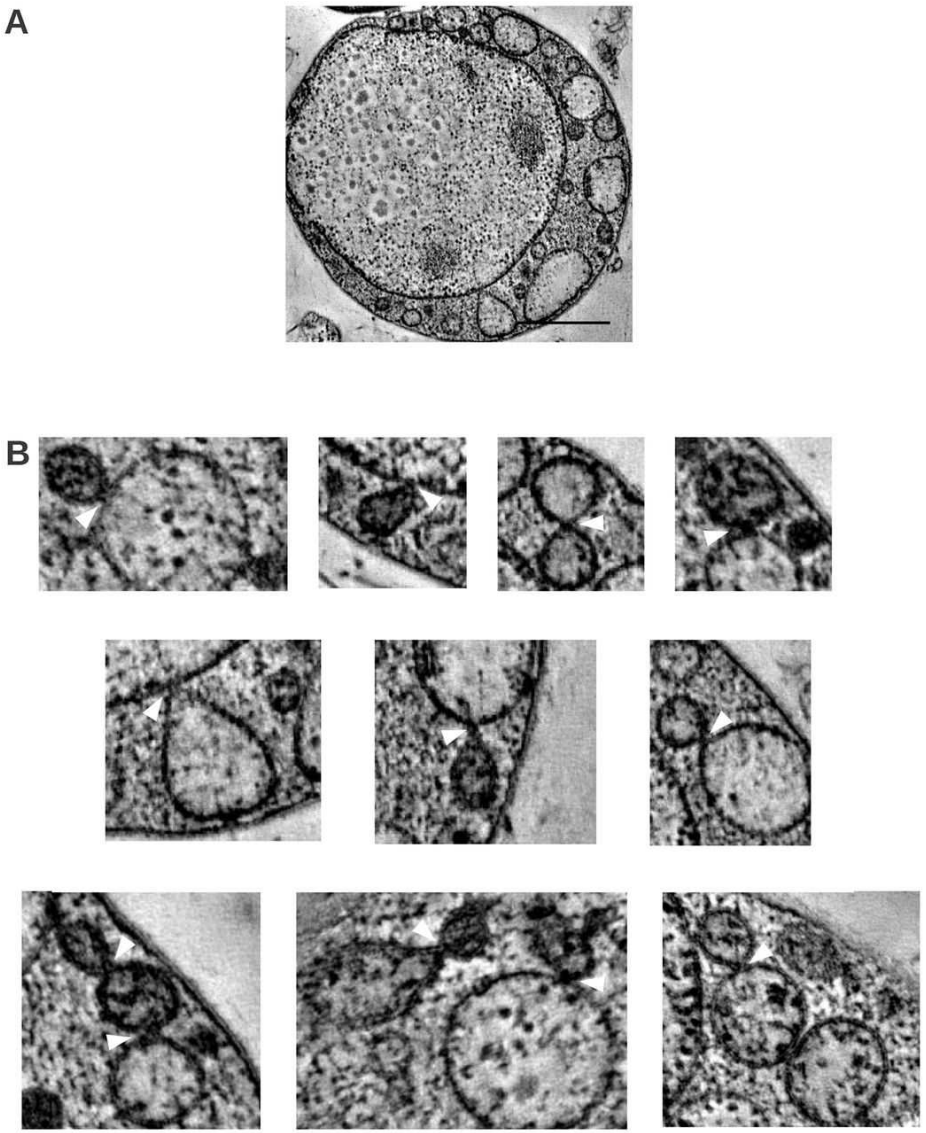
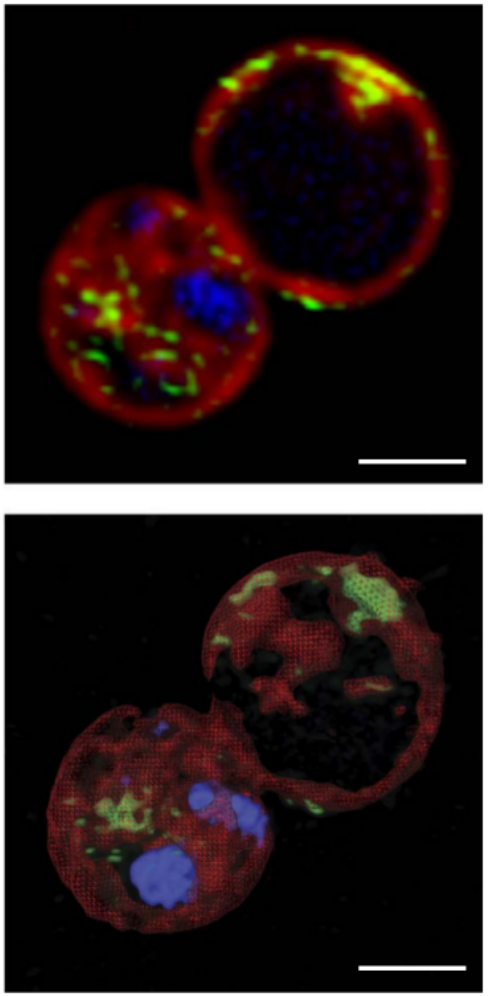
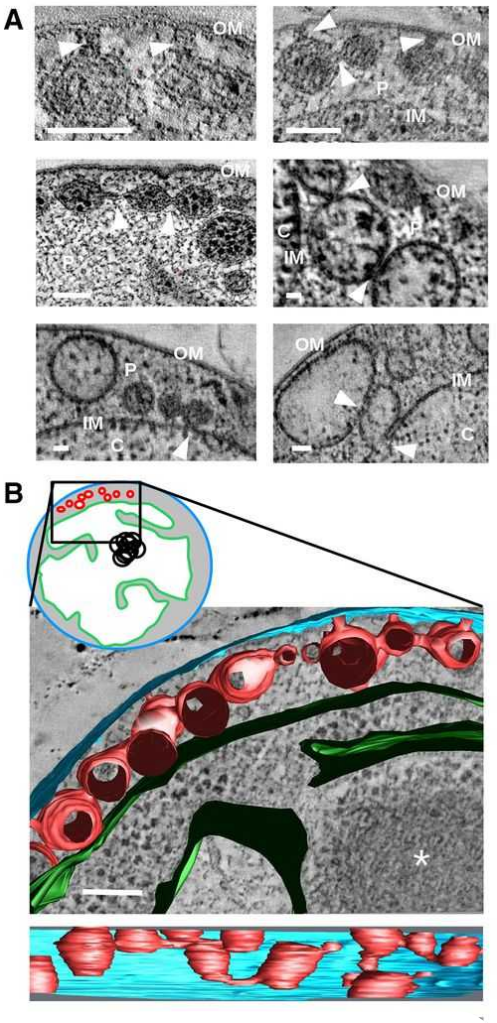
- Evolution: Diverse group of bacteria
  - 'Ancestral' bacteria or Long Branch Atraction? Rapid evolution?
  - How was diversity generated from Last PVC Common Ancestor (LPCA)?
- Cell biology
  - Endomembrane system (how? When, dynamic?)
  - Membrane coat proteins (link with eukaryotes → LGT?)
  - Tubulovesicular network
- Link to human (and animal) health
  - Verrucomicrobia and Planctomycetes
- Earth system
  - Including kelp
- Bioproduction and bioremediation

Prokaryotic connected vesicles

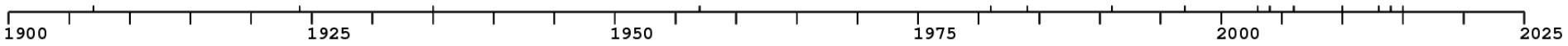






Acehan *et al.*, JCS 2014; Boedeker *et al.*, Nat Coms 2017

PVC timeline

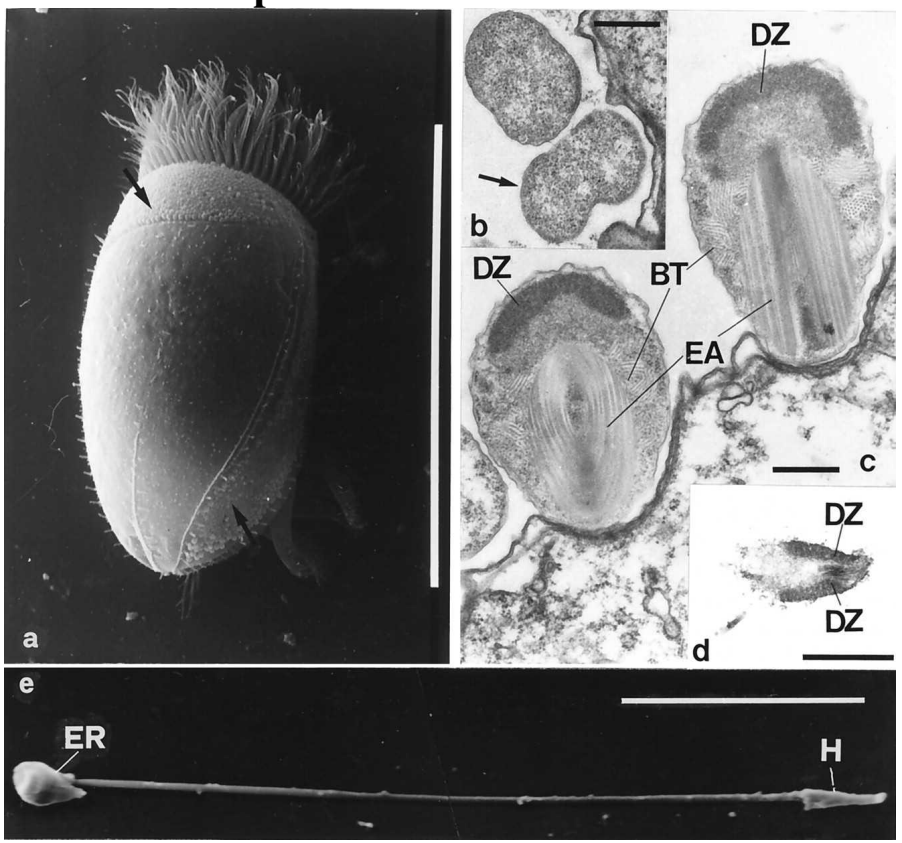


Coexistence of Tubulins and *ftsZ* in Different *Prosthecobacter* Species

Martin Pilhofer, Giovanna Rosati, Wolfgang Ludwig, Karl-Heinz Schleifer, Giulio Petroni

Mol Biol Evol (2007) 24 (7): 1439-1442. **DOI:** https://doi.org/10.1093/molbev/msm069

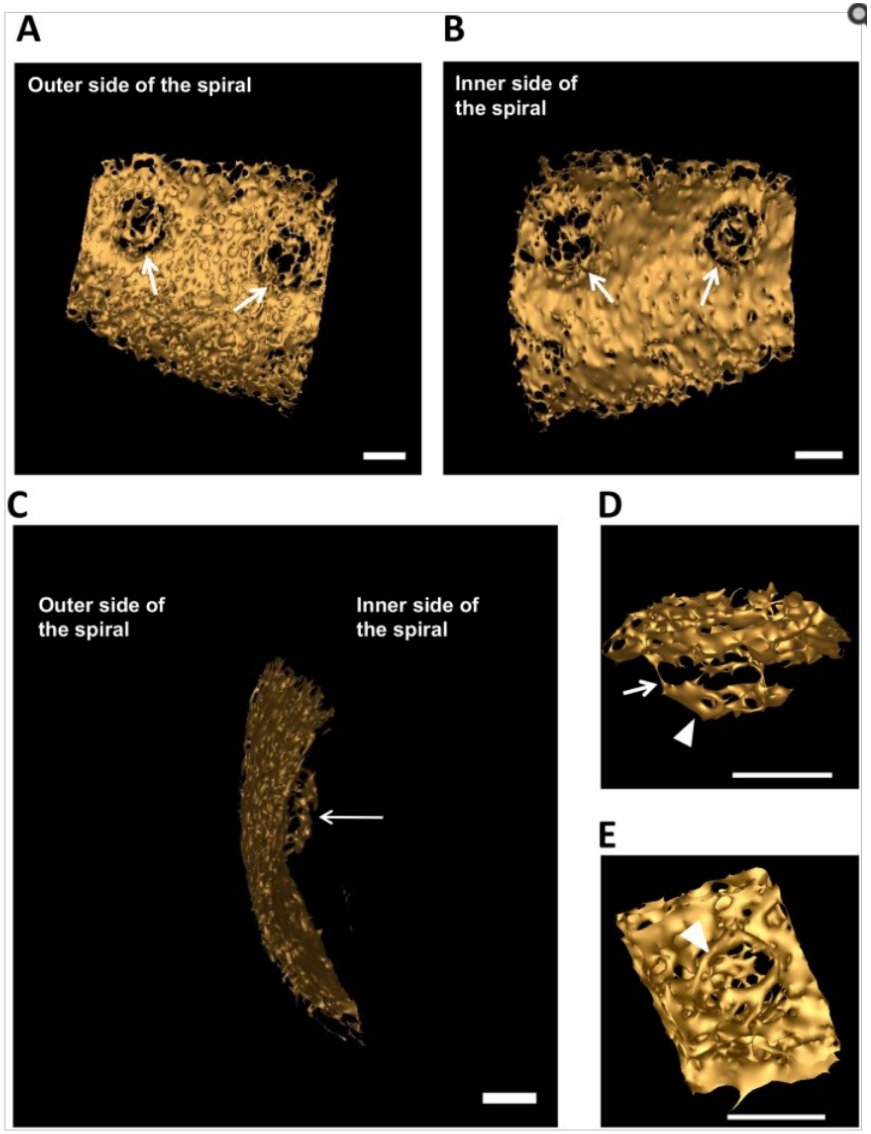
Epixenosomes and their host.



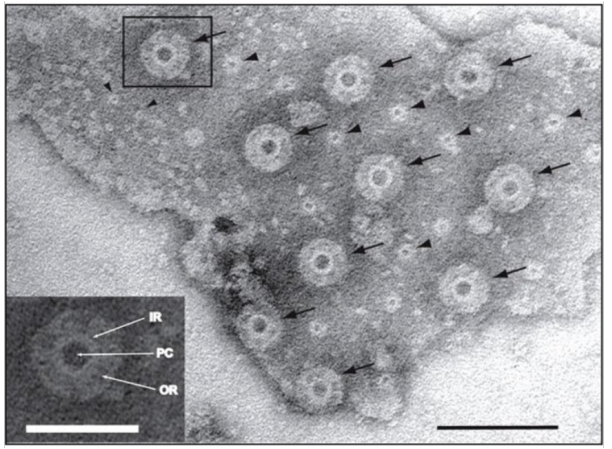
Defensive extrusive ectosymbionts of Euplotidium (Ciliophora) that contain microtubule-like structures are bacteria related to Verrucomicrobia

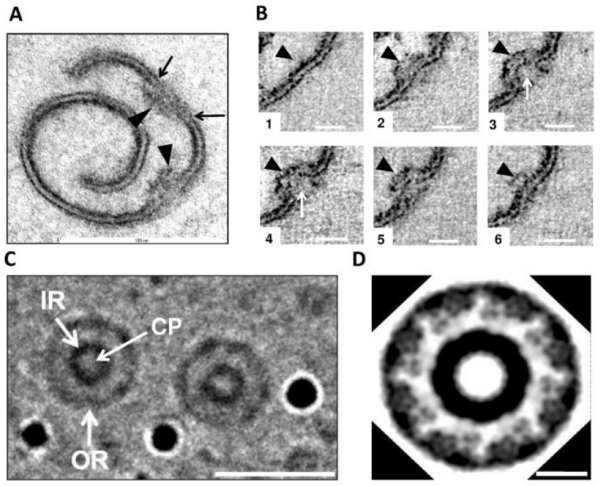
Petroni et al. PNAS 2000

The bacterial pore complex



3-D reconstructions of the pore complex.





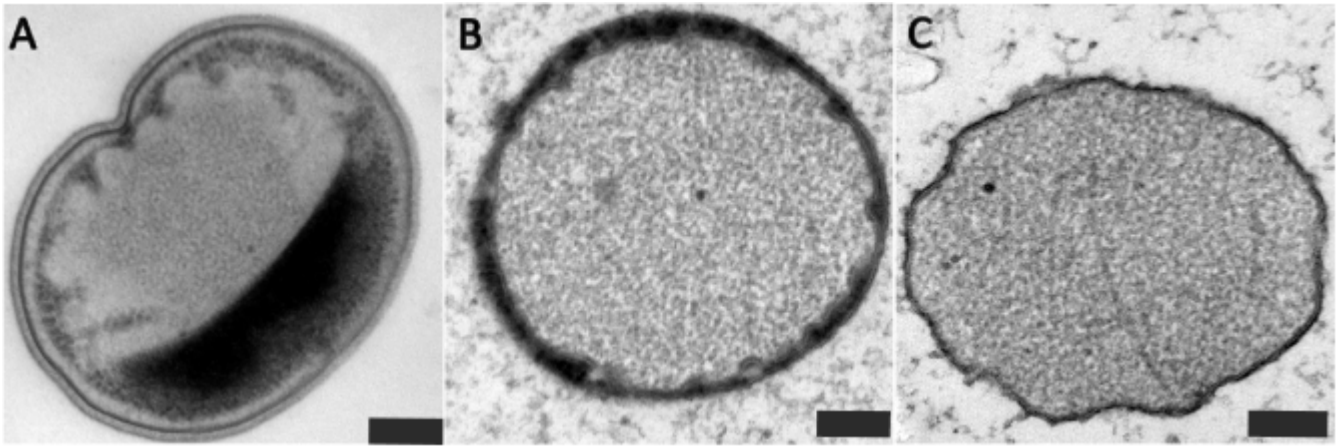
Sagulenko et al., PLoS One (2017)

The bacterial 'mitochondrion'

Jogler

Centro Andaluz de Biología del Desarrollo

Isolation and characterization of a prokaryotic cell organelle
from the anammox bacterium *Kuenenia stuttgartiensis*



Neumann *et al*. Mol Micro 2014

Underestimation due to primer bias

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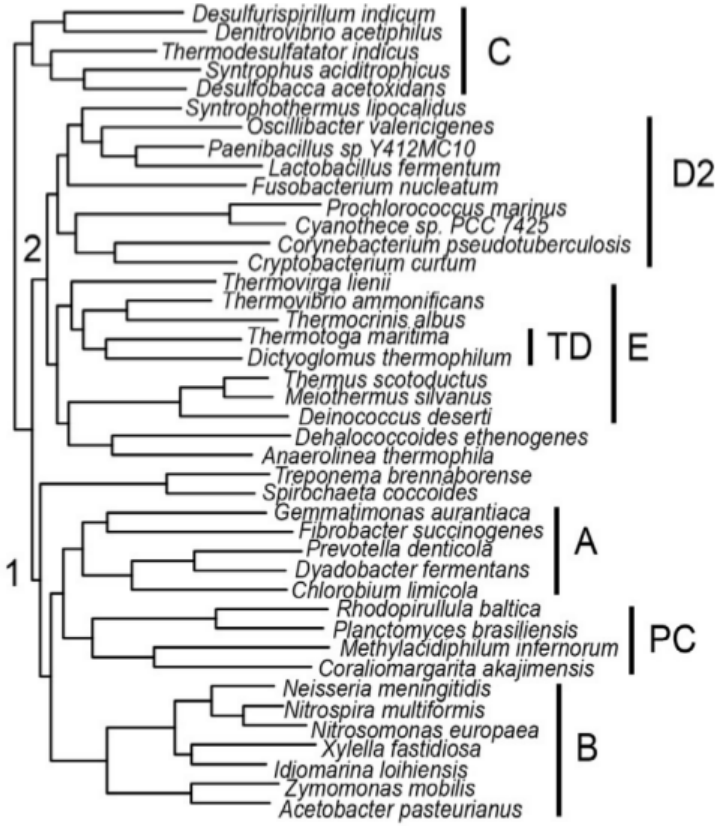
The under-recognized dominance of *Verrucomicrobia* in soil bacterial communities

Gaddy T. Bergmann[a, b], Scott T. Bates[a, b], Kathryn G. Eilers[a, b], Christian L. Lauber[a, b], J. Gregory Caporaso[c], William A. Walters[d], Rob Knight[c, e], Noah Fierer[a, b]

Verrucomicrobia were detected in 180 out of 181 soils examined, with members of the class Spartobacteria dominating verrucomicrobial communities in nearly all biomes and soil depths. The relative abundance of Verrucomicrobia was highest in grasslands and in subsurface soil horizons, where they were often the dominant bacterial phylum. Although their ecology remains poorly understood, **Verrucomicrobia** appear to be **dominant in many soil bacterial communities** across the globe, making additional research on their ecology clearly necessary.



some bacterial relationships were always recovered and strongly supported regardless of the model implemented such as a Chlamydiae/Planctomycetes clade (PC), a Fibrobacteria, Bacteriodetes, Chlorobi + Gemmatimonadetes monophyly (labeled clade ‘‘A’’ in Fig. 4), a Proteobacteria (Alpha, Beta, and Gamma) + Nitrospirae group (or clade ‘‘B’’ in Fig. 4) and a Deferribacteres, Chrysiogenetes, Thermodesulfobacteria, + Delta/Epsilon Proteobacteria clade (clade ‘‘C’’ in Fig. 4).

Lasek-Nesselquist and Gogarten (2013) MPE

Last PVC Common Ancestor (LPCA)

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From an evolutionary perspective, two chlamydia-like bacteria deserve special attention, the uncultured “Candidatus Piscichlamydia salmonis” and “Candidatus Clavochlamydia salmonicola.” “Ca. Piscichlamydia salmonis” is particularly interesting because it currently represents the **deepest branch in the Chlamydiae**, i.e., it might still share **features of the last common ancestor** of all chlamydiae, which are absent in all other chlamydial lineages. “Ca. Clavochlamydia salmonicola” is the closest relative of the Chlamydiaceae (Figure 1) and might thus represent a **transitional stage** between the highly adapted human and animal pathogens of the Chlamydiaceae and all other chlamydia-like bacteria. Novel approaches and technologies such as whole-genome amplification and pyrosequencing might facilitate genome analysis of these organisms in the near future.

Horn, Ann Rev Micro 2008

PVC integrative computational biology

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PVCBASE

An online resource for the PVC Bacteria Community

Home | About | Contact | BLAST Webserver | PVCwiki

*By **Juan Carlos Gonzalez Sanchez** (juancarlosgonzs@gmail.com) and **Nicola Bordin** (nbor1@upo.es)*
Centro Andaluz de Biología del Desarrollo. Universidad Pablo de Olavide. Sevilla
1 May 2015

http://pvcbacteria.org/pvcbase/

submitted

Gemmata obscuriglobus UQM2246 tax214688 NCBI 7756prt (7756 proteins)

The proteins sequeneces in FASTA format used in this analysis can be downloaded here .

The complete table is also available in .tsv format for downloading.

Show 10 entries

Search:

NAME / ID	Description	Organism	Protein Length (aa)	Best PSIBLAST Hit: Uniprot Accession [+stats]	Best PSIBLAST Hit: Gene	Best PSIBLAST Hit: Description	Best PSIBLAST Hit: GO terms	Best PSIBLAST Hit: Keywords	Best PSIBLAST Hit: EC number	Signal_Peptide	TMHs	Disorder % [Globular Domains]	InterPro Entry	InterPro: pathways	InterPro: GO terms - Molecular Function	InterPro: GO terms - Biological Proccess	InterPro: GO terms - Cellular Component
gi|497718965|ref|WP_010033149.1|	ATP-dependent helicase	Gemmata obscuriglobus	700	Q6AZV7 [Cov=81.7% Evalue=8e-164]	ddx55	ATP-dependent RNA helicase DDX55	GO:0005524; F:ATP binding; IEA:UniProtKB-KW.GO:0004386; F:helicase activity; IEA:UniProtKB-KW.GO:0003723; F:RNA binding; IEA:UniProtKB-KW.	ATP-binding; Coiled coil; Helicase; Hydrolase; Nucleotide-binding;RNA-binding.	EC=3.6.4.13	-	0 [SP=n, topology=o]	2.86 % [GlobDoms= (1-700)]	IPR011545: DEAD/DEAH box helicase domain	-	GO:0005524: ATP binding; GO:0003676: nucleic acid binding	-	-

Search:

InterPro: GO terms - Biological Proccess	InterPro: GO terms - Cellular Component	InterPro: Pfam	InterPro: TIGRFAM	InterPro: PANTHER	InterPro: ProSiteProfiles	InterPro: Hamap	InterPro: PIRSF	InterPro: Gene3D	InterPro: SUPERFAMILY	InterPro: PRINTS	InterPro: SMART	HHblits vs Uniprot20 annotation	HHpred (vs PDB)
-	-	PF00270: DEAD/DEAH box helicase; PF00271: Helicase conserved C-terminal domain	-	PTHR24031:SF176: SUBFAMILY NOT NAMED; PTHR24031: FAMILY NOT NAMED	PS51194: Superfamilies 1 and 2 helicase C-terminal domain profile." name="HELICASE_CTER; PS51192: Superfamilies 1 and 2 helicase ATP-binding type-1 domain profile." name="HELICASE_ATP_BIND_1	-	-	G3DSA:3.40.50.300; G3DSA:3.40.50.300	SSF52540: P-loop containing nucleoside triphosphate hydrolases	-	SM00490: helicase superfamily c-terminal domain; SM00487: DEAD-like helicases superfamily	ATP-dependent helicase [Cov=99.1% Prob=100.0 Evalue=9E-132]; DEAD/DEAH box helicase-like [Cov=99.1% Prob=100.0 Evalue=9E-132]; DEAD/DEAH box helicase domain protein [Cov=99.1% Prob=100.0 Evalue=9E-132];	2va8_A (3-452) SSO2462, SKI2-type helicase; hydrolase, DNA repair, ATP-bindin nucleotide-binding; [Prob=100.0 Evalue=3.2E-49]; 2p6r_A (6-451) Afuhel308 helicase; protein-DNA complex, SF2 helicase, archaeal helicase, DNA repair,, DNA binding protein/DNA complex; [Prob=100.0 Evalue=4.9E-49]; 2zj8_A (7-452) DNA helicase, putative SKI2-type helicase; RECA fold, ATP-binding, hydrolase, nucleotide- binding; [Prob=100.0 Evalue=8.7E-49]; 2db3_A (3-354) ATP-dependent RNA helicase VASA; DEAD-BOX, protein-RNA complex, ATPase, riken structural genomics/proteomics initiative, RSGI; HET: ANP; [Prob=100.0 Evalue=8.6E-47];

PVC integrative computational biology

Centro Andaluz de Biología del Desarrollo

*By **Juan Carlos Gonzalez Sanchez** (juancarlosgonzs@gmail.com) and **Nicola Bordin** (nbor1@upo.es)*
Centro Andaluz de Biología del Desarrollo. Universidad Pablo de Olavide. Sevilla
1 May 2015

http://pvcbacteria.org/pvcbase/

Gemmata obscuriglobus UQM2246 tax214688 NCBI 7756prt (7756 proteins)

The proteins sequeneces in FASTA format used in this analysis can be downloaded here .

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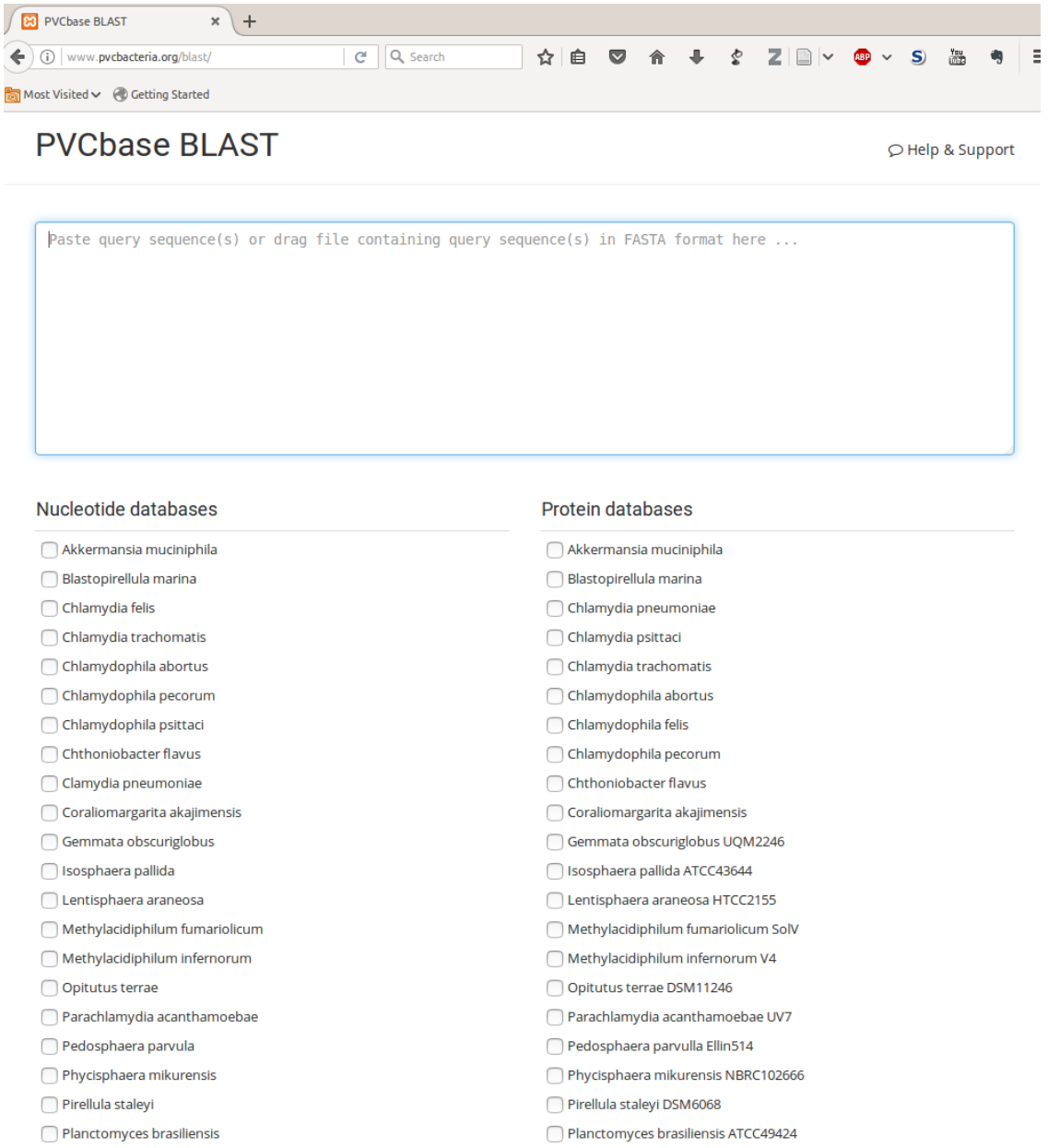
NAME / ID	Description	Organism	Protein Length (aa)	Best PSIBLAST Hit: Uniprot Accession [+stats]	Best PSIBLAST Hit: Gene	Best PSIBLAST Hit: Description	Best PSIBLAST Hit: GO terms	Best PSIBLAST Hit: Keywords	Best PSIBLAST Hit: EC number	Signal_Peptide	TMHs	Disorder % [Globular Domains]	InterPro Entry	InterPro: pathways	InterPro: GO terms - Molecular Function	InterPro: GO terms - Biological Proccess	InterPro: GO terms - Cellular Component
gi|497718906|ref|WP_010033090.1|	hypothetical protein, partial	Gemmata obscuriglobus	1537	-	-	-	-	-	-	-	-		0 [SP=n, topology=o]	53.29 % [GlobDoms= (626-992) (1268-1537)]	IPR028974: TSP type-3 repeat	-	

Search:

InterPro: GO terms - Biological Process	InterPro: GO terms - Cellular Component	InterPro: Pfam	InterPro: TIGRFAM	InterPro: PANTHER	InterPro: ProSiteProfiles	InterPro: Hamap	InterPro: PIRSF	InterPro: Gene3D	InterPro: SUPERFAMILY	InterPro: PRINTS	InterPro: SMART	HHblits vs Uniprot20 annotation	HHpred (vs PDB)
-	-	-	-	-	-	-	-	-	-	-	-	GO:0005509: calcium ion binding; GO:0005509: calcium ion binding; GO:0005509:	-
8974: pe-3	-	GO:0005509: calcium ion binding; GO:0005509: calcium ion binding; GO:0005509: calcium ion binding	-	-	-	-	-	PS00018: EF-hand calcium-binding domain." name="EF_HAND_1	-	-	G3DSA:4.10.1080.10	SSF103647: TSP type-3 repeat; SSF103647: TSP type-3 repeat	-	-	Thrombospondin type 3 repeat [Cov=24.9% Prob=100.0 Evalue=5.6E-69]; Predicted calcium-binding protein [Cov=32.5% Prob=100.0 Evalue=2E-113];	3fby_A (1007-1361) COMP, cartilage oligomeric matrix protein; signature domain, cell adhesion, disease mutation, dwarfism, EGF-like domain, glycoprotein, secreted; HET: NAG MAN; [Prob=99.9 Evalue=8.8E-25]; 1yo8_A (935-1253) Thrombospondin-2; EGF, Ca(2+)-binding domains, lectin domain, disulfide, cell; HET: NAG MAN; [Prob=99.9 Evalue=5.5E-23]; 1ux6_A (1067-1212) Thrombospondin-1; extracellular matrix, calcium binding, L-type lectin, glycoprotein, cell adhesion, calcium-binding, heparin-binding; [Prob=99.3 Evalue=3.7E-12]; 2j42_A (422-763) C2-II, C2 toxin component-II; [Prob=98.3 Evalue=4.3E-07];

PVC blast


PVCbase BLAST
www.pvcbacteria.org/blast/
Search
Most Visited
Getting Started
PVCbase BLAST
Help & Support
Paste query sequence(s) or drag file containing query sequence(s) in FASTA format here ...
Nucleotide databases
Akkermansia muciniphila
Blastopirellula marina
Chlamydia felis
Chlamydia trachomatis
Chlamydophila abortus
Chlamydophila pecorum
Chlamydophila psittaci
Chthoniobacter flavus
Clamydia pneumoniae
Coraliomargarita akajimensis
Gemmata obscuriglobus
Isosphaera pallida
Lentisphaera araneosa
Methylacidiphilum fumariolicum
Methylacidiphilum infernorum
Opitutus terrae
Parachlamydia acanthamoebae
Pedosphaera parvula
Phycisphaera mikurensis
Pirellula staleyi
Planctomyces brasiliensis
Protein databases
Akkermansia muciniphila
Blastopirellula marina
Chlamydia pneumoniae
Chlamydia psittaci
Chlamydia trachomatis
Chlamydophila abortus
Chlamydophila felis
Chlamydophila pecorum
Chthoniobacter flavus
Coraliomargarita akajimensis
Gemmata obscuriglobus UQM2246
Isosphaera pallida ATCC43644
Lentisphaera araneosa HTCC2155
Methylacidiphilum fumariolicum SolV
Methylacidiphilum infernorum V4
Opitutus terrae DSM11246
Parachlamydia acanthamoebae UV7
Pedosphaera parvulla Ellin514
Phycisphaera mikurensis NBRC102666
Pirellula staleyi DSM6068
Planctomyces brasiliensis ATCC49424

2020?

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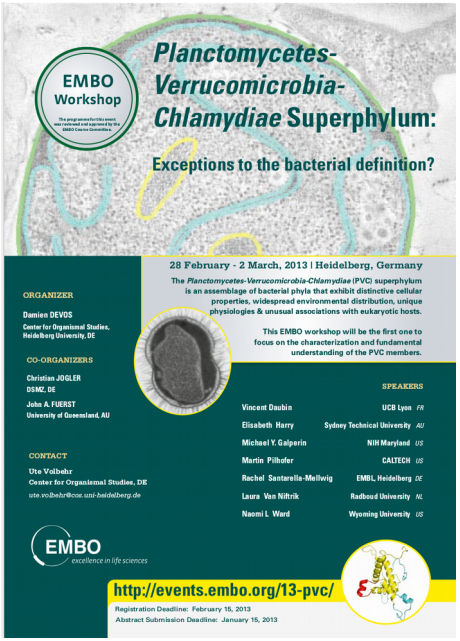

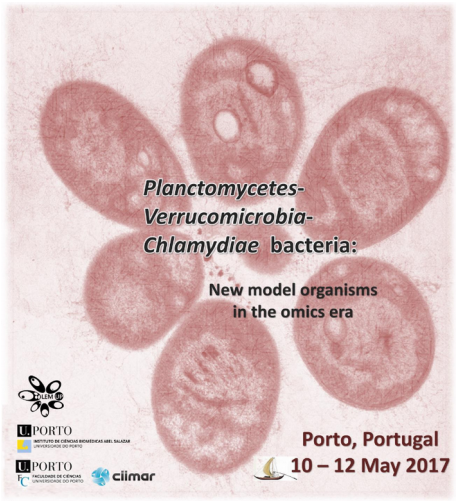

Nijmegen?

Lausanne?

Previous PVC meetings
Heidelberg, DE 2013 - Sevilla, SP 2015

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43 participants; 8 keynotes
16 countries

Antonie Van Leeuwenhoek. 2013 Oct;104(4):443-9. doi: 10.1007/s10482-013-0026-y. Epub 2013 Sep 20.

The 1st EMBO workshop on PVC bacteria-Planctomycetes-Verrucomicrobia-Chlamydiae superphylum: exceptions to the bacterial definition?

Devos DP[1], Jogler C, Fuerst JA.

27 participants; 4 keynotes
10 countries

frontiers

Topic Editors

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Damien Paul Devos
CABD, Uni. Pablo Olavide, Sevilla, Spain

Research Topic

Planctomycetes-Verrucomicrobia-Chlamydiae bacterial superphylum: New model organisms!